

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:00:29 ; Search time 2253.73 Seconds
(without alignments)
1983.487 Million cell updates/sec

Title: US-09-698-903B-10

Perfect score: 416

Sequence: 1 ctacggcaatgtaccagctg.....catgaacacccaaactcgat 416

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estfun: *
2: em_esthum: *
3: em_estin: *
4: em_estom: *
5: em_estpl: *
6: em_estba: *
7: em_estro: *
8: em_estov: *
9: em_hic: *
10: gb_est1: *
11: gb_est2: *
12: gb_hic: *
13: gb_gss: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pln: *
18: em_gss_pro: *
19: em_gss_rod: *
20: em_gss_vrt: *
21: em_gss_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	63.2	15.2	734	13	CNS010MP
C 2	58.8	14.1	1101	13	CNS00238
C 3	56.6	13.6	1101	13	CNS0042W
C 4	55.8	13.4	537	13	AQ506817
C 5	55.6	13.4	421	13	AQ917446
C 6	55.4	13.3	300	13	AQ098895
C 7	55.2	13.3	844	13	CNS03D0I
C 8	55.2	13.3	845	13	AQ745337
C 9	55.2	13.3	1101	13	CNS00K47
C 10	55	13.2	980	13	CNS00JG1
C 11	54.8	13.2	928	13	CNS00DKY
C 12	54.8	13.2	980	13	CNS00JG1

13	54.6	13.1	1101	13	CNS00EVL
14	54.4	13.1	678	13	CNS02A0C
15	53.8	12.9	1337	5	BF630719
C 16	53.6	12.9	1101	13	CNS003BA
C 17	53.2	12.8	340	10	AL514737
C 18	53.2	12.8	1101	13	CNS003BB
C 19	53.2	12.8	1203	13	CNS015WU
C 20	53	12.7	421	13	AQ917446
C 21	53	12.7	1101	13	CNS00EYK
C 22	53	12.7	1169	13	CNS006HQ
C 23	52.8	12.7	725	13	AQ917102
C 24	52.8	12.7	1141	13	CNS07206
C 25	52.6	12.6	1101	13	CNS00E07
C 26	52.6	12.6	1101	13	CNS00EVL
C 27	52.4	12.6	697	13	CNS04707
C 28	52.4	12.6	725	13	AQ917102
C 29	52.4	12.6	1101	13	CNS001FB
C 30	52.2	12.5	458	10	AU086681
C 31	52.2	12.5	500	10	AU086078
C 32	52.2	12.5	1101	13	CNS00B01
C 33	52.2	12.5	1101	13	CNS0161I
C 34	51.8	12.5	1101	13	CNS00FMC
C 35	51.6	12.4	377	13	AQ012444
C 36	51.6	12.4	711	13	AQ051188
C 37	51.4	12.4	1101	13	CNS0039G
C 38	51.4	12.4	1225	13	CNS0161D
C 39	51.2	12.3	517	13	AZ929020
C 40	51.2	12.3	1085	13	CNS02PW4
C 41	51	12.3	340	10	AL514737
C 42	51	12.3	764	13	AQ915359
C 43	51	12.3	1101	13	CNS0161I
C 44	50.8	12.2	500	10	AU086152
C 45	50.6	12.2	901	13	AZ551119

ALIGNMENTS

RESULT 1
LOCUS CNS010MP/c

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL099163.1 GI:5610774

VERSION AL099163.1

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 734)

GENOSCOPE

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Genoscope.

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pheloBAC11.

FEATURES

Location/Qualifiers

1..734

/organism="Drosophila melanogaster"

/plasmid="pBelobAC11"

/db_xref="taxon:7227"

/clone_lib="DrosBAC"

/clone="BACN04L20"

source

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BASE COUNT      288 a      62 c      2 g      211 t      171 others
ORIGIN

Query Match      15.2%; Score 63.2; DB 13; Length 734;
Best Local Similarity 41.2%; Pred. NO. 0.008;
Matches 84; Conservative 43; Mismatches 77; Indels 0; Gaps 0;

Qy 21 atataacagttattgaattctggaatttctgaatttctgacatcaataaawttatgtttt 80
Db 259 ATAWWWWWKTTTITTKWATATKTTTWTAAATTAATAATAATTTTWTWTWTWTWTWT 200

Qy 81 gcttggaactaatacctgactgttcttcttcttcttcttcttcttcttcttcttctt 140
Db 199 WKTTTWTAAWAAAAATWTRAKKWWTTTAAATAATTTTAAATKAAAAATATWTTK 140

Qy 141 caagatgggaattacatctcaataatgcctttcttcttcttcttcttcttcttcttctt 200
Db 139 DAAAAKAAAAATWATATWTWKDWTAWTTTWTWTWTWTWTWTWTWTWTWTWTWTWT 80

Qy 201 aattataattataattataata 224
Db 79 ATWATTWTATATAATATAATA 56

RESULT 2
LOCUS      CNS00238      1101 bp      DNA      GSS      26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
ACCESSION  AL097166
VERSION     AL097166
KEYWORDS   GSS.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  1 (bases 1 to 1101)
AUTHORS   Direct Submission
TITLE     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL   BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelOBAC11.

FEATURES             Location/Qualifiers
     source           1..1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBelOBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN01A24"
                     /note="end : SP6"

BASE COUNT      308 a      152 c      162 g      386 t      93 others
ORIGIN

Query Match      14.18; Score 58.8; DB 13; Length 1101;
Best Local Similarity 41.9%; Pred. NO. 0.051;
Matches 88; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

Qy 21 atataacagttattgaattctggaatttctgacatcaataaawttatgtttt 80
Db 829 AWTWTARDDDKKKAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 888

BASE COUNT      288 a      62 c      2 g      211 t      171 others
ORIGIN

Query Match      15.2%; Score 63.2; DB 13; Length 734;
Best Local Similarity 41.2%; Pred. NO. 0.008;
Matches 84; Conservative 43; Mismatches 77; Indels 0; Gaps 0;

Qy 81 gcttggaactaatacctgactgttcttcttcttcttcttcttcttcttcttcttctt 140
Db 889 TTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 948

Qy 141 caagatgggaattacatctcaataatgcctttcttcttcttcttcttcttcttcttctt 200
Db 949 AAAAAAATAAAAAATWAAAAATTTTWTATATAAAAAATATWAAATWAAW 1008

Qy 201 aattataattataattataataactgaaa 230
Db 1009 APTAAAAATAAAAAATTWAAATAAAWAAW 1038

RESULT 3
LOCUS      CNS0042W      1101 bp      DNA      GSS      03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
ACCESSION  BACR11E08 of RPCI-98 library from Drosophila melanogaster (fruit
VERSION     BACR11E08 of RPCI-98 library from Drosophila melanogaster (fruit
KEYWORDS   fly), genomic survey sequence.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  1 (bases 1 to 1101)
AUTHORS   Direct Submission
TITLE     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL   BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammos in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            ECORI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            p1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES             Location/Qualifiers
     source           1..1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR11E08"
                     /note="end : T7"

BASE COUNT      294 a      74 c      99 g      381 t      253 others
ORIGIN

Query Match      13.6%; Score 56.6; DB 13; Length 1101;
Best Local Similarity 38.3%; Pred. NO. 0.13;
Matches 147; Conservative 50; Mismatches 186; Indels 1; Gaps 1;

Qy 20 gatataacagttattgaatttctggaatttctgacatcaataaawttatgtttt 79
Db 695 DAAATATATAMACAKTWTAKATTTTAAAKTAAAAAAWAAWAAWAAWAAWAAWAAW 754

Qy 80 tgccttggaactaatacctgactgttcttcttcttcttcttcttcttcttcttcttctt 139
Db 755 WATWTAATAATWAAWTAATATATATWTTTWTWTWTWTWTWTWTWTWTWTWTWTWT 814

Qy 140 tcaagatgggaattacatctcaataatgcctttcttcttcttcttcttcttcttcttctt 199

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Db 815 TATATATAAGAAVAATATWTTAAATWAAATANTATANTATATATATTTAAATTTATTCA 874
QY 200 taattataataattataactgaactgaacaccggtgccccctgctgcttaccatgga 259
Db 875 TWAATAATAATTTTAAATATTAATWAAATAAATAATWTTTAAATATATWTTTAAATTT 934
QY 260 ttctcgcgtactattgtatatacgtatataatataccgtata-atgcatatatttatat 318
Db 935 TKTTATWTTAMDATWTTATTTATATATWTTAAATAAATAAATAAATAAATAAATAAATA 994
QY 319 gaacatataatgctgtgagttgtctcatcgtaagagtttcaataatgtaagtga 378
Db 995 WTAAATAAAATWTTATTTTGTGTAAATAATWTTAAATAATWTTTAAATAATATA 1054
QY 379 agagtcacaaaccccaatcatgaa 402
Db 1055 AAKTTTAAATWAAATWAAAW 1078

RESULT 4
AQ506817 537 bp DNA GSS 29-APR-1999
LOCUS RPCI-11-281J17-TV RPCI-11 Homo sapiens genomic clone RPCI-11-281J17
DEFINITION , DNA sequence.
ACCESSION AQ506817
VERSION AQ506817.1 GI:4711564
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI-11-281J17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: bheetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufoalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufoalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tadb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .537
/organism="Homo sapiens"
/db_xref="GDB:7607752"
/db_xref="taxon:9606"
/clone="RPCI-11-281J17"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"
BASE COUNT 216 a 11 c 30 g 280 t
ORIGIN

Query Match 13.4%; Score 55.8; DB 13; Length 537;
Best Local Similarity 48.5%; Pred. No. 0.21;
Matches 150; Conservative 1; Mismatches 158; Indels 0; Gaps 0;

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QY 21 atataacagttattgaataatttctgaatttaaaccttgcatcaataaawttatgttttt 80
Db 99 ATATATGATATATTTGATATATATTTATATATATATATATATATATATATATATATAT 158
QY 81 gctgggactataacacctgacctgtttattttatcaataaataatttaaacactatattcttt 140
Db 159 TTATATATATGATATATATATATATATATATATATATATATATATATATATATATAT 218
QY 141 caagatgggaataacatctacaaatgcctttcttctatcgaccatgtacatccctacac 200
Db 219 ATATATTTGATATATATATATATATATATATATATATATATATATATATATATATAT 278
QY 201 aattataataattataataactgaacaccatgggtgccccctgctgcttaccatggat 260
Db 279 ATATATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 338
QY 261 ttctccgctactattgtatataacgtatataacgtataaataatgcatatatttatatga 320
Db 339 GTATATATTTATATATATATATATATATATATATATATATATATATATATATATATAT 398
QY 321 acatgatta 329
Db 399 ATATATTTTA 407

RESULT 5
AQ917446/c 421 bp DNA GSS 07-DEC-1999
LOCUS T233481b Medicago truncatula BAC library Medicago truncatula
DEFINITION genomic clone 15E22, DNA sequence.
ACCESSION AQ917446
VERSION AQ917446.1 GI:6537021
KEYWORDS GSS.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 421)
AUTHORS Kim,D., Limpens,E., Peng,H., Ellis,L. and Cook,D.R.
TITLE BAC end sequencing of Medicago truncatula
JOURNAL Unpublished (1999)
COMMENT Contact: Cook DR
The Crop Biotechnology Center
Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120 L.F.
Peterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 8743
Fax: 409 862 4790
Email: dcook@ppserver.tamu.edu
Other name: DK457-L; date: 8/12/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 12/06/99; More information is
available at 'http://chrystie.tamu.edu/medicago'.
Seq primer: SQ-BAC-L (AACGCCAGGGTTTCCCGAGTCACGACG)
Class: BAC ends.
FEATURES
source
1. .421
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="15E22"
/clone_lib="Medicago truncatula BAC library"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII; Nam. Y-W, Penmetza, R.V., Endre, G., Kim, D., and
Cook, D.R. 1999. Construction of a bacterial artificial
chromosome library of Medicago truncatula and
identification of clones containing ethylene response
genes. Theor Appl Genet 98: 638-646."
BASE COUNT 191 a 19 c 5 g 205 t
ORIGIN

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Query Match	13.4%	Score 55.6	DB 13	Length 421	
Best Local Similarity	48.1%	Pred. No. 0.24			
Matches	154	Conservative	1	Mismatches 165	Indels 0
Gaps	0				
QY	21	atataatcagttgattgaataatttcgaatttaaaactgcatcaataaaawttatgttttt	80		
DB	362	AT	303		
QY	81	gcttggaacttaataacacgtcgaatttcattttatcaataaataattttaaactatattctt	140		
DB	302	AT	243		
QY	141	caagtgagggaatttaaacatctcaacaaattgccttttcttatcgaccatgcatcaccat	200		
DB	242	AT	183		
QY	201	aattataaattataataataactgaactgaacacgtggtgccccgtgctgtttacatgat	260		
DB	182	AT	123		
QY	261	ttctccgcacatttgcatacgtgtatatataccgtataatgaatgacatatattttatga	320		
DB	122	CTCTCAT	63		
QY	321	acatgatttaactgctgtgag	340		
DB	62	ATATATATATAGAGAGAG	43		
RESULT	6				
LOCUS	AQ098895	300 bp	DNA	GSS	27-AUG-1998
DEFINITION	HS 3050_AL_C03_MR C1F Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=5 Row=E, DNA sequence.				
ACCESSION	AQ098895				
VERSION	AQ098895.1	GI:3469924			
KEYWORDS	GSS.				
SOURCE	Human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 300)				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.				
JOURNAL	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3050 row: E column: 5 Class: BAC ends High quality sequence stop: 300. Location/Qualifiers				
FEATURES	1..300				
source	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="plate=3050 Col=5 Row=E"				
	/sex="male"				
	/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"				
BASE COUNT	150 a	8 c	4 g	138 t	
ORIGIN					

```
Query Match      13.3%; Score 55.2; DB 13; Length 844;
Best Local Similarity 46.4%; Pred. No. 0.26;
Matches 153; Conservative 7; Mismatches 170; Indels 0; Gaps 0;

QY 31 ttattgaataatttcgaatttaaaactgcatcaataaaattatgttttttgcctggacta 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 TGAATTTAAATGTTTATGATTTTATTTTATAGAGTAAAGTTATATATTTTATTCCTTTTAA 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 91 taacacactgactgttatttatacaataaataatttaaacatattcttccaagatggga 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 TTTTATATKTATATATTTTATTTTATTTTATTTTATATKTTTATTTTATATCATTTAK 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 ataacatctacaaatgccttttcttcacgcacatgcacatccacacataattataatt 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 GTTTTAKATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 ataattataataactgaacacatgggccccctgcctgttcacatgagatttcccgcta 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 TTTTWTAAATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 ctattgtacgctgtatataacgcgtataatgtacatatatttataatgaacatgattaa 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 TAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 tgcctgtgagttgtcttcacccgtaagagt 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 458 TTTTATTTACTTGTATTATATGCGCAACACT 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
AQ745537/c      845 bp      DNA      GSS      16-JUL-1999
LOCUS      HS_2272.A2.B12.T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION      sapiens genomic clone Plate=2272 Col=24 Row=C, DNA sequence.
ACCESSION      AQ745537
VERSION      AQ745537.1 GI:5523059
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 845)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
               Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
               Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
               scanning the human genome
JOURNAL      Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE      99380589
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu
               Clones may be purchased from Research Genetics (info@resgen.com).
               BAC end Web Server: http://www.htsc.washington.edu
               Plate: 2272 row: C column: 24
               Seq primer: T7
               Class: BAC ends
               High quality sequence stop: 845.
FEATURES      Location/Qualifiers
               source      1..845
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone="Plate=2272 Col=24 Row=C"
                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
                   /sex="male"
                   /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                   E-Coli DH10B"
BASE COUNT      360 a 114 c 93 g 278 t
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;
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ORIGIN

```
Query Match      13.3%; Score 55.2; DB 13; Length 845;
Best Local Similarity 47.9%; Pred. No. 0.26;
Matches 156; Conservative 1; Mismatches 169; Indels 0; Gaps 0;

QY 39 atattctgaatttaaaactgcatcaataaaattatgttttttgcctggactataaact 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 ATATATATATATTTTATATATTTTATATATATTTTATATATATTTTATATATATTTT 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 99 gactgttattttcaataaataatttaaacatataatttcttccaagatgggaataaacat 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 ATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATAT 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 ctacaaattgccttcttctatcgaccatgctacacctaccataattataataaattat 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 TTATATATATTTTATATATTTTATATATTTTATATATATTTTATATATTTTATAT 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 219 ataatactgaacacatggtgccccctgcctgttcacatggattcttcgcgtactattgt 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 ATATATTTTATATATTTTATATTTTATATATATTTTATATATATTTTATATATATAT 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 279 atacgtgtatatataccgataaagtacatatatttatgaacatgattaatgcttg 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 TTATATATATTTTATATATTTTATATTTTATATATATTTTATATATATATATATAT 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 339 agttgttctcatccgtaagagtttca 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 ATACATGATAAAATGCGAGACTTCCA 33
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
CNS00K47      1101 bp      DNA      GSS      03-JUN-1999
LOCUS      Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION      BACR39E17 of RPCI-98 library from Drosophila melanogaster (fruit
               fly), genomic survey sequence.
ACCESSION      AL077203
VERSION      AL077203.1 GI:4956680
KEYWORDS      GSS.
SOURCE      fruit fly.
ORGANISM      Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
               Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 1101)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
               BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
               - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
               collaboration with the Berkeley Drosophila Genome Project (BDGP).
               The BDGP is constructing a physical map of the Drosophila
               melanogaster genome using these BACs. For further information
               please see http://www.fruitfly.org The BDGP Drosophila
               melanogaster BAC library was prepared by Kazutoyo Osoegawa and
               Aaron Mamoser in Pieter de Jong's laboratory in the Department of
               Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
               NY. The library is named RPCI-98 and was constructed by partial
               EcoRI digestion of Drosophila DNA provided by the BDGP from the
               isogenic strain y2; cn bw sp, the same strain used for the BDGP's
               pl and EST libraries. A more detailed description of the library
               and how to order individual BAC clones, the entire library, or
               filters for hybridization from the BACPAC Resource Center can be
               found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES      Location/Qualifiers
               source      1..1101
                   /organism="Drosophila melanogaster"
                   /db_xref="taxon:7227"
                   /clone_lib="RPCI-98"
                   /clone="BACR39E17"
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BASE COUNT 314 a 99 c 73 g 489 t 126 others
ORIGIN

Query Match 13.3%; Score 55.2; DB 13; Length 1101;
Best Local Similarity 42.1%; Pred. No. 0.25;
Matches 144; Conservative 7; Mismatches 191; Indels 0; Gaps 0;

QY 21 atataacagttattgaattctgaatttcaactgtcatcaataaawttatgtttt 80
DB 306 ATATATATCTCTATTTTATATGATATCGTNTATNTATCTCTATATATATNT 365
QY 81 gcttgactataacacgtgctgtttattttatcaataaaattttaaactattcttt 140
DB 366 CTCTTTTAT 425
QY 141 caagatgggaataacactcaaaattcccttttcttccatgaccatgtacatccat 200
DB 426 AT 485
QY 201 aattataattataatgactgtgtatataacgtataatgactgtgtatgactgtat 260
DB 486 NTNTCTATTTTCTCTATATATTTTNTNGTATATATATATATATATATATATAT 545
QY 261 ttctcgcctactattgtatataacgtgtatataacgtataatgactgtatgactgtat 320
DB 546 ATATTTCTTTATCTAT 605
QY 371 acatgattaatgctgtgagtggttctccatcgtaagagttt 362
DB 606 ATATNATNT 647

RESULT 10
CNS00JG1

LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC: 03-JUN-1999
DEFINITION BACR38J18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL076232
VERSION AL076232.1 GI:4955810
KEYWORDS GSS.

SOURCE fruit fly.
ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS 1 (bases 1 to 980)
JOURNAL Genoscope.

COMMENT Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

1..980
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

/clone_lib="RPCI-98"
/clone="BACR38J18"
/notes="end : T7"

BASE COUNT 400 a 112 c 102 g 297 t 69 others
ORIGIN

Query Match 13.2%; Score 55; DB 13; Length 980;
Best Local Similarity 41.9%; Pred. No. 0.27;
Matches 142; Conservative 37; Mismatches 155; Indels 5; Gaps 1;

QY 21 atataacagttattgaattctgaatttcaactgtcatcaataaawttatgtttt 80
DB 586 AT 645
QY 81 gcttgactataacacgtgactgtttattttatcaataaattttaaactattcttt 140
DB 646 AT 705
QY 141 caagatgggaataacactcaaaattgcttcttctatcgaccatgtacatccat 200
DB 706 TWTWTAT 765
QY 201 aattataattataatgactgtgtatataacgtgtatataacgtgtgtgtgtgtgt 260
DB 766 ATTATAAAAT 820
QY 261 ttctcgcctactattgtatataacgtgtatataacgtgtatataacgtgtatata 320
DB 821 TWCAGTTTAAATTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTT 880
QY 321 acatgattaatgctgtgagtggttctccatcgtaagag 359
DB 881 GTARAADWADARRRRTTRARGRTTTTTTTTGTGKGGGG 919

RESULT 11
CNS00DKY

LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC: 04-JUN-1999
DEFINITION BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL071865
VERSION AL071865.1 GI:4948170
KEYWORDS GSS.

SOURCE fruit fly.
ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS 1 (bases 1 to 928)
JOURNAL Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

1..928


```
CC Tel: 864 656 7288
CC Fax: 864 656 4293
CC Email: rwing@clemons.edu
CC Seq primer: AATTAAACCTCACTAAAGGG
CC High quality sequence start: 38
CC High quality sequence stop: 1204.
XX
FH Key Location/Qualifiers
FH
FT source 1..1337
FT /db_xref="taxon:4513"
FT /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
FT /organism="Hordeum vulgare"
FT /cultivar="Morex"
FT /clone="HVSMEb0013H16f"
FT /clone_lib="Hordeum vulgare seedling shoot EST library
FT HVCdNA002 (Dehydration stress)"
FT /tissue_type="Seedling shoot"
FT /lab_host="TJC121"
XX
SQ Sequence 1337 BP; 292 A; 22 C; 74 G; 941 T; 8 other;

Query Match      12.9%; Score 53.8; DB 5; Length 1337;
Best Local Similarity 51.2%; Pred. No. 0.44;
Matches 147; Conservative 1; Mismatches 135; Indels 4; Gaps 1;

QY 38 aatattctgaattaaacttgcataaataaattatgttttcttgctggactataacc 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 851 ATTATTTTATGATATTAATCTTATCATCTGTTTTTTTGCTCTTTTATTTATT 910
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 98 tgacttgattttatcaataaataattaaactatattcttccaagatgggaattaaca 157
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 911 TTAGTTATTTATTTATTTATGATATTTATTTATTTATTTATTTATTTATTTAT 966
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 158 tctacaaattgcctttcttctatcgaccatgacatccctaccataaattataatta 217
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 967 TCATTATTTATTTTATTTTATTTTATTTTATTTATTTATTTATTTATTTATTTA 1026
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 218 tataactactgaaccatgggccccctgccttgcttacatggattctccgctactattg 277
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1027 TTTATTTGTTTTTTTATTTTCATATTTTGATATTTATTTATTTATTTATTTATTTGT 1086
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 278 tatacgtgtatatataccgtataatgtacatatatttataatgaacat 324
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1087 ATTTATTTATTTATTTATTTATTTTANTATTTGTTATTTATTTATTTATTTAT 1133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: December 19, 2001, 17:00:33
Job time: 2275 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

QM nucleic - nucleic search, using sw model

Run on December 19, 2001, 17:31:51 ; Search time 230.16 Seconds
(without alignments)
1549.562 Million cell updates/sec

Title: US-09-698-903B-10
Perfect score: 416
Sequence: 1 ctacggcaatgtaccagctg.....catgaacaccccaactcgat 416

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
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red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415.6	99.9	416	22	Left (3') border
2	380.8	91.5	415	22	Right (5') border
3	192.6	46.3	5864	17	Plasmid pTCS113 T-
4	192.6	46.3	5865	22	Chimeric T-DNA of
5	192.6	46.3	7599	22	Nucleotide sequenc
6	190	45.7	5228	22	Plasmid pTCS172del
7	190	45.7	6539	21	E. coli plasmid pT
8	190	45.7	6548	17	Plasmid pTCS174 use
9	190	45.7	6548	18	Plasmid pTCS172. C
10	190	45.7	6548	21	E. coli plasmid pT
11	190	45.7	7492	22	Plasmid pTCS346. U

12	189.6	45.6	1303	17	AAT39337	Plasmid pTCS88 (Eco
13	189.6	45.6	3201	12	AAQ14529	pPS029 Bt ICP codi
14	189.6	45.6	4832	22	AAH25423	Nucleotide sequenc
15	189.6	45.6	4946	18	AAT59531	T-DNA of plasmid p
16	189.6	45.6	4946	22	AAH25422	Nucleotide sequenc
17	189.6	45.6	5349	19	AAV23339	T-DNA of pTCS24.
18	189.6	45.6	5864	17	AAT39339	Plasmid pTCS113 T-
19	189.6	45.6	5865	22	AAH25423	Chimeric T-DNA of
20	189.6	45.6	7566	14	AAQ42160	Plasmid pPS0212 co
21	189.6	45.6	7639	14	AAQ42159	Plasmid pJD884 con
22	183.6	44.1	1037	11	AAQ04705	USP-promoter-casse
23	183.6	44.1	1085	11	AAQ04703	Legumin-signalpept
24	183.6	44.1	1160	11	AAQ04706	USP-signalpeptide
25	179	43.0	1077	22	AAH25439	Right flanking reg
26	176.6	42.5	3201	12	AAQ15144	pVE36 Bt ICP codin
27	152.6	36.7	1186	13	AAQ25707	Chimeric neo gene
28	145.6	35.0	3153	21	AAZ29122	Plasmid pV131 comp
29	145.6	35.0	3336	21	AAZ29121	Plasmid pV130 comp
30	145.6	35.0	3694	21	AAZ29124	Plasmid pV133 used
31	145.6	35.0	3877	21	AAZ29123	Plasmid pV132 used
32	145.6	35.0	24593	6	AAH50182	Sequence of opine
33	145.6	35.0	24596	6	AAH50182	Complete nucleotid
34	104.6	25.1	936	22	AAF58252	Oligonucleotide D1
35	104.6	25.1	936	22	AAF58254	Oligonucleotide D1
36	104.6	25.1	936	22	AAF58257	Oligonucleotide D1
37	104.6	25.1	936	22	AAF58259	Oligonucleotide D2
38	104.6	25.1	936	22	AAF58262	Oligonucleotide D2
39	104.6	25.1	938	22	AAF58255	Oligonucleotide D1
40	104.2	25.0	936	22	AAF58252	Oligonucleotide D1
41	104.2	25.0	936	22	AAF58254	Oligonucleotide D1
42	104.2	25.0	936	22	AAF58257	Oligonucleotide D1
43	104.2	25.0	936	22	AAF58259	Oligonucleotide D2
44	104.2	25.0	936	22	AAF58262	Oligonucleotide D2
45	104.2	25.0	938	22	AAF58255	Oligonucleotide D1

ALIGNMENTS

RESULT	1
AAD06999	
ID	AAD06999 standard; DNA; 416 BP.
XX	
AC	AAD06999;
DT	
DT	06-AUG-2001 (first entry)
XX	
DE	Left (3') border flanking region of elite event MS-B2.
XX	
KW	MS-B2 elite event; transgenic Brassica plant; transformation event;
KW	male-sterility gene; ds.
XX	
OS	Chimeric - Agrobacterium sp.
OS	Chimeric - Brassica sp.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 1..193
FT	/tag= a
FT	/note= "Corresponds to T-DNA"
FT	misc_feature 194..416
FT	/tag= b
FT	/note= "Corresponds to plant DNA"
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XX	WO200131042-A2.
PN	
XX	03-MAY-2001.
PD	
XX	26-OCT-2000; 2000WO-EP10680.
PF	
XX	29-OCT-1999; 99US-0430497.
PR	
XX	(AVET) AVENTIS CROPS SCIENCE NV.
PA	
XX	

```

PI Weston B, De Beuckeleer M;
XX WPI; 2001-300517/31.
XX
XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
XX harboring specific transformation events, particularly by presence of
XX male-sterility gene, at specific location in its genome.
XX
XX Claim 11; Page 52; 53pp; English.
XX
XX The present invention relates to a transgenic Brassica plant or its
XX seed, cells or tissues, characterised by harbouring a specific
XX transformation event, particularly by the presence of a male-sterility
XX gene, at a specific location in the Brassica genome. Transgenic
XX Brassica plant is useful for producing a hybrid seed by crossing the
XX transgenic plant with a male-fertile Brassica plant and harvesting the
XX hybrid seed from the transgenic Brassica plant.
XX The present sequence is left (3') border flanking region of elite event
XX MS-B2.
XX
XX Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;

Query Match          99.9%; Score 415.6; DB 22; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtacacgtgataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 1 ctacggcaatgtacacgtgataatcagttattgaaatatttctgaatttaaaacttgc 60
QY 61 atcaataaaawttatgttttcttgctggactataataacotgactgttattttatcaataaa 120
Db 61 atcaataaaawttatgttttcttgctggactataataacotgactgttattttatcaataaa 120
QY 121 tatttaactatattttcttcaagatgggaattaaacatctacaaatgcctttcttattc 180
Db 121 tatttaactatattttcttcaagatgggaattaaacatctacaaatgcctttcttattc 180
QY 181 gaccatgtacatctacacataataataattataataataactgaacacccatggtgc 240
Db 181 gaccatgtacatctacacataataataattataataataactgaacacccatggtgc 240
QY 241 cctgtgctttacatggattttctcgcactactatttggatagtgatataataccgtata 300
Db 241 cctgtgctttacatggattttctcgcactactatttggatagtgatataataccgtata 300
QY 301 atgtacatatatttatgaacatgattaatgcttggagtggtttctcgcactacgtata 360
Db 301 atgtacatatatttatgaacatgattaatgcttggagtggtttctcgcactacgtata 360
QY 361 ttcaatatgtaatgggtgaagagtcacaaacccaaatcattgaacacccaaactcgat 416
Db 361 ttcaatatgtaatgggtgaagagtcacaaacccaaatcattgaacacccaaactcgat 416

RESULT 2
AAD06997/C
ID AAD06997 standard; DNA; 415 BP.
XX
XX AAD06997;
XX
XX 06-AUG-2001 (first entry)
XX
XX Right (5') border flanking region of elite event MS-B2.
XX
XX MS-B2 elite event; transgenic Brassica plant; transformation event;
XX male-sterility gene; ds.
XX
XX Chimeric - Agrobacterium sp.
XX Chimeric - Brassica sp.
XX
XX Key Location/Qualifiers

```

```

FT misc_feature 1..234
FT FT /*tag= a
FT FT /note= "Corresponds to plant DNA"
FT misc_feature 235..415
FT FT /*tag= b
FT FT /note= "Corresponds to T-DNA"
XX
XX WO200131042-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-EP10680.
XX
XX 29-OCT-1999; 99US-0430497.
XX
XX (AVET ) AVENTIS CROPS SCIENCE NV.
XX
XX Weston B, De Beuckeleer M;
XX
XX WPI; 2001-300517/31.
XX
XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
XX harboring specific transformation events, particularly by presence of
XX male-sterility gene, at specific location in its genome.
XX
XX Claim 11; Page 51; 53pp; English.
XX
XX The present invention relates to a transgenic Brassica plant or its
XX seed, cells or tissues, characterised by harbouring a specific
XX transformation event, particularly by the presence of a male-sterility
XX gene, at a specific location in the Brassica genome. Transgenic
XX Brassica plant is useful for producing a hybrid seed by crossing the
XX transgenic plant with a male-fertile Brassica plant and harvesting the
XX hybrid seed from the transgenic Brassica plant.
XX The present sequence is right (5') border flanking region of elite event
XX MS-B2.
XX
XX Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;

Query Match          91.5%; Score 380.8; DB 22; Length 415;
Best Local Similarity 98.5%; Pred. No. 1.4e-67;
Matches 404; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 1 ctacggcaatgtacacgtgataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 415 ctacggcaatgtacacgtgataatcagttattgaaatatttctgaatttaaaacttgc 60
QY 61 atcaataaaawttatgttttcttgctggactataataacotgactgttattttatcaataaa 120
Db 355 atcaataaaawttatgttttcttgctggactataataacotgactgttattttatcaataaa 296
QY 121 tatttaactatattttcttcaagatgggaattaaacatctacaaatgcctttcttattc 180
Db 295 tatttaactatattttcttcaagatgggaattaaacatctacaaatgcctttcttattc 236
QY 181 gaccatgtacatctacacataataataattataataataactgaacacccatggtgc 239
Db 235 gaccatgtacatctacacataataataattataataataactgaacacccatggtgc 176
QY 240 cctgtgctttacatggattttctcgcactactatttggatagtgatataataccgtata 299
Db 175 cctgtgctttacatggattttctcgcactactatttggatagtgatataataccgtata 117
QY 300 aatgtacatatatttatgaacatgattaatgcttggagtggtttctcgcactacgtata 359
Db 116 aatgtacatatatttatgaacatgattaatgcttggagtggtttctcgcactacgtata 57
QY 360 ttcaatatgtaatgggtgaagagtcacaaacccaaatcattgaacacccaaactcgat 409
Db 56 ttcaatatgtaatgggtgaagagtcacaaacccaaatcattgaacacccaaactcgat 7

```

RESULT 3

AAT39339 standard; DNA; 5864 BP.

AC AAT39339;

DT 22-JAN-1997 (first entry)

XX Plasmid pTCO113 T-DNA used to obtain male sterile oilseed rape.

DE Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar;

KW transgenic plant; oilseed rape; canole; Brassica napus; ds.

XX Synthetic.

OS

XX Key Location/Qualifiers

FH complement (1..25)

FT /*tag= a

FT /label= RB

FT /note= "right border of Agrobacterium T-DNA"

FT complement (98..330)

FT /*tag= b

FT /label= 3'g7

FT /note= "region containing polyA signal of gene 7

FT of Agrobacterium T-DNA"

FT complement (331..882)

FT /*tag= c

FT /label= bar

FT /note= "region coding for phosphinothricin

FT acetyltransferase"

FT complement (883..2608)

FT /*tag= d

FT /label= Pssu

FT /note= "promoter of Arabidopsis Rubisco small

FT subunit gene"

FT complement (2659..3031)

FT /*tag= e

FT /label= 3'nos

FT /note= "region containing polyA signal of nopaline

FT synthase gene of Agrobacterium T-DNA"

FT complement (3032..3367)

FT /*tag= f

FT /label= Barnase

FT /note= "Bacillus amyloliquefaciens barnase coding

FT region"

FT complement (3368..4877)

FT /*tag= g

FT /label= PTA29

FT /note= "promoter of stamen-specific TA29 gene of

FT Nicotiana tabacum"

FT 4924..5216

FT /*tag= h

FT /label= Pnos

FT /note= "promoter of nopaline synthase gene of

FT Agrobacterium T-DNA"

FT 5217..5489

FT /*tag= i

FT /label= Barstar

FT /note= "region coding for barstar of Bacillus

FT amyloliquefaciens"

FT 5490..5765

FT /*tag= j

FT /label= 3'g7

FT /note= "region containing polyA signal of gene 7

FT of Agrobacterium T-DNA"

FT complement (5840..5864)

FT /*tag= k

FT /label= LB

FT /note= "left border of Agrobacterium T-DNA"

FT

XX misc_feature

PN W09626283-A1.

XX 29-AUG-1996.

XX 21-FEB-1996; 96WO-EP00722.

XX 21-FEB-1995; 95EP-0400364.

XX (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Botterman J, Cornelissen M, Michiels F;

PI WPI; 1996-402373/40.

DR Prodn. of male sterile plants by transforming with a chimaeric

XX construct - comprising a male sterility DNA e.g. barnase and a

PT co-regulating gene, e.g. barstar, into the nuclear genome, useful

PT for generating hybrid cultivars

XX Example 3; Page 33-3743-47; 56pp; English.

XX Plasmid pTCO113 (AAT39339) is a T-DNA vector containing a bar gene

CC under control of the PSSU promoter, a barnase gene under control

CC of the stamen-specific PTA29 promoter, and a barstar (co-regulatory)

CC gene under control of the Pnos promoter. 87% Of oilseed rape

CC plants regenerated after Agrobacterium-mediated transformation

CC using pTCO113 were male sterile. Barnase expression disturbed the

CC function of stamen cells leading to male sterility. Constitutive

CC expression of barstar counteracted any low level expression of

CC barnase in non-stamen tissue.

XX Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;

SQ

Query Match 46.3%; Score 192.6; DB 17; Length 5864;

Best Local Similarity 99.5%; Pred. No. 4.6e-30;

Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaattaaacttgc 60

DB 5620 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaattaaacttgc 5679

QY 61 atcaataaaatgtattttgtcttggaactataataacacctgactgttatttcaataaa 120

DB 5680 atcaataaaatgtattttgtcttggaactataataacacctgactgttatttcaataaa 5739

QY 121 tatttaactatatttttccaagatgggaattacaactacaatgcctttttttatc 180

DB 5740 tatttaactatatttttccaagatgggaattacaactacaatgcctttttttatc 5799

QY 181 gaccatgtacatc 193

DB 5800 gaccatgtacatc 5812

RESULT 4

AAD06990

ID AAD06990 standard; DNA; 5865 BP.

XX

AC AAD06990;

XX

DT 06-AUG-2001 (first entry)

XX Chimeric T-DNA of plasmid pTCO113.

DE T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event;

DE male-sterility gene; chimeric; tobacco; ds.

XX

KW Chimeric - Streptomyces hygroscopicus.

OS Chimeric - Arabidopsis thaliana.

OS Chimeric - Bacillus amyloliquefaciens.

OS Chimeric - Nicotiana tabacum.

OS Chimeric - Agrobacterium tumefaciens.

OS Chimeric - Unidentified.

XX Key Location/Qualifiers

FH

```
FT misc_feature 1..25
FT /tag= a
FT /note= "Right border repeat from the TL-DNA from
FT ptIB6S3"
FT 26..53
FT /tag= b
FT /note= "Synthetic polylinker derived sequence"
FT 54..90
FT /tag= c
FT /note= "Residual sequence from the TL-DNA at the
FT right border repeat"
FT 98..309
FT /tag= d
FT /note= "The 3' untranslated end from the TL-DNA
FT gene 7 (3'g7) of ptIB6S3"
FT 310..331
FT /tag= e
FT /note= "Synthetic polylinker derived sequence"
FT 332..883
FT /tag= f
FT /product= "Protein encoded by bialaphos resistance
FT gene (bar) of Streptomyces hygroscopicus"
FT 884..2609
FT /tag= g
FT /note= "Promoter from the atSIA ribulose-1,5-biphosphate
FT carboxylase small subunit gene from Arabidopsis thaliana"
FT 2610..2659
FT /tag= h
FT /note= "Synthetic polylinker derived sequence"
FT 2660..2920
FT /tag= i
FT /note= "TagI fragment from the 3' untranslated end of the
FT nopaline synthase gene (3'nos) from the T-DNA of pTiT37
FT and containing plant polyadenylation signals"
FT 2921..2936
FT /tag= j
FT /note= "Synthetic polylinker derived sequence"
FT 2937..3032
FT /tag= k
FT /note= "The 3' untranslated region downstream from the
FT barnase coding sequence of Bacillus amyloliquefaciens"
FT 3033..3368
FT /tag= l
FT /product= "Protein encoded by barnase gene from
FT Bacillus amyloliquefaciens"
FT 3369..4878
FT /tag= m
FT /note= "Promoter region of the anther-specific gene
FT TA29 from Nicotiana tabacum"
FT 4879..4924
FT /tag= n
FT /note= "Synthetic polylinker derived sequence"
FT 4925..5215
FT /tag= o
FT /note= "Promoter of the nopaline synthase gene from the
FT T-DNA of pTiT37 of Agrobacterium tumefaciens"
FT 5216..5217
FT /tag= p
FT /note= "Synthetic polylinker derived sequence"
FT 5218..5490
FT /tag= q
FT /product= "Protein encoded by barstar gene of
FT Bacillus amyloliquefaciens"
FT 5491..5530
FT /tag= r
FT /note= "Sequence from the 3' untranslated end of the
FT barstar gene from Bacillus amyloliquefaciens"
FT 5531..5554
FT /tag= s
FT /note= "Synthetic polylinker derived sequence"
FT 5555..5766
FT /tag= t
FT /note= "The 3' untranslated end from the TL-DNA
```

```
FT misc_feature gene 7 (3'g7) of ptIB6S3"
FT 5767..5773
FT /tag= u
FT /note= "Synthetic polylinker derived sequence"
FT 5774..5810
FT /tag= v
FT /note= "Residual sequence from the TL-DNA at the
FT right border repeat"
FT 5811..5840
FT /tag= w
FT /note= "Synthetic polylinker derived sequence"
FT 5841..5865
FT /tag= x
FT /note= "Left border repeat from the TL-DNA from
FT ptIB6S3"
FT WO200131042-A2.
FT PN
FT 03-MAY-2001.
FT PD
FT 26-OCT-2000; 2000WO-EP10680.
FT PF
FT 29-OCT-1999; 99US-0430497.
FT PR
FT (AVET ) AVENTIS CROPS SCIENCE NV.
FT PA
FT Weston B, De Beuckeleer M;
FT PI
FT WPI; 2001-300517/31.
FT DR
FT XX
FT Transgenic Brassica plants, seeds, cells or tissues, characterized by
FT harboring specific transformation events, particularly by presence of
FT male-sterility gene, at specific location in its genome -
FT XX
FT Claim 1; Page 47-49; 53pp; English.
FT XX
FT The present invention relates to a transgenic Brassica plant or its
FT seed, cells or tissues, characterised by harbouring a specific
FT transformation event, particularly by the presence of a male-sterility
FT gene, at a specific location in the Brassica genome. Transgenic
FT Brassica plant is useful for producing a hybrid seed by crossing the
FT transgenic plant with a male-fertile Brassica plant and harvesting the
FT hybrid seed from the transgenic Brassica plant.
FT The present sequence is chimeric T-DNA of plasmid pTCO113. This sequence
FT comprises right border repeat, left border repeat and 3' untranslated
FT region (UTR) from TL-DNA of ptIB6S3, synthetic polylinker sequences,
FT coding regions of bialaphos resistance gene (bar) from
FT streptomyces hygroscopicus, barnase gene from Bacillus amyloliquefaciens
FT and barstar gene from Bacillus amyloliquefaciens and promoters of atSIA
FT ribulose-1,5-biphosphate carboxylase small subunit gene from
FT Arabidopsis thaliana, the anther-specific gene TA29 from
FT Nicotiana tabacum and nopaline synthase gene from the T-DNA of pTiT37
FT of Agrobacterium tumefaciens.
FT XX
FT Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
```

```
Query Match 46.3%; Score 192.6; DB 22; Length 5865;
Best Local Similarity 99.5%; Pred. No. 4.6e-30;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaataattctgaattcaacttgc 60
Db 5621 ctacggcaatgtaccagctgataataatcagttattgaaataattctgaattcaacttgc 5680

QY 61 atcaataaaawttatgtttttgttgaggactataataacacctgacttattttatcaataaa 120
Db 5681 atcaataaaawttatgtttttgttgaggactataataacacctgacttattttatcaataaa 5740

QY 121 tatttaaaactattttcttccaagatgggaattacaactacaatctcaaatgcctttcttctatc 180
Db 5741 tatttaaaactattttcttccaagatgggaattacaactacaatctcaaatgcctttcttctatc 5800
```

```
QY 181 gaccatgtacatc 193
Db 5801 gaccatgtacatc 5813

RESULT 5
AAF25320
ID AAF25320 standard; DNA; 7599 BP.
XX
AC AAF25320;
DT
XX
XX 30-APR-2001 (first entry)
DE
XX Nucleotide sequence of a plasmid pGKB5.
XX
XX Plant promoter; root cell; root-specific expression; parasite resistance;
KW nematode resistance; fungal resistance; water stress; salt stress;
KW sugar content; nitrogen transport; ss.
XX
OS Synthetic.
XX
XX WO200100833-A1.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 23-JUN-2000; 2000WO-FR01768.
PF
XX
XX 25-JUN-1999; 99FR-0008185.
PR
XX
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA
XX Hoffmann B, Mollier P, Pelletier G;
PI
XX WPI; 2001-102893/11.
DR
XX
XX New constitutive plant promoter active specifically in roots, useful
PT for controlling expression of pest or drought resistance genes, and
PT related transgenic plants -
XX
XX Disclosure; Fig 9; 92pp; French.
XX
XX The present sequence represents a plasmid pGKB5. The plasmid contains
CC a plant promoter that directs expression of a selected sequence in
CC root cells at all stages of development of a plant. The plant promoter
CC is used to control expression of genes in a root-specific manner,
CC especially genes that provide resistance to parasites, pests (nematodes
CC or fungi), water and salt stress, or alter sugar content or nitrogen
CC transport. Fragments of the promoter are useful as probes or primers
CC to detect or amplify at least part of the promoter.
XX
SQ Sequence 7599 BP; 1972 A; 1938 C; 1937 G; 1752 T; 0 other;

Query Match 46.3%; Score 192.6; DB 22; Length 7599;
Best Local Similarity 99.5%; Pred. No. 4.6e-40;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 60
Db 6579 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 6638

QY 61 atcaataaaawttatgttttctgttgactataataacacctgactgttattttatcaataaa 120
Db 6639 atcaataaaawttatgttttctgttgactataataacacctgactgttattttatcaataaa 6698

QY 121 tatttaaacatattttcttcaagatggggaattaaacatctacaattgcctttcttctatc 180
Db 6699 tatttaaacatattttcttcaagatggggaattaaacatctacaattgcctttcttctatc 6758

QY 181 gaccatgtacatc 193
Db 6759 gaccatgtacatc 6771
```

```
RESULT 6
AAF86439
ID AAF86439 standard; DNA; 5228 BP.
XX
AC AAF86439;
XX
DT 25-JUN-2001 (first entry)
XX
XX Plasmid pTSl72delta.
DE
XX Male sterile plant; RNase inhibitor; plasmid pTSl72delta; ds.
XX
XX Unidentified.
OS
XX WO200124616-A1.
PN
XX 12-APR-2001.
PD
XX 12-SEP-2000; 2000WO-JP06222.
PF
XX 30-SEP-1999; 99JP-0279307.
PR
XX (NISB ) JAPAN TOBACCO INC.
PA
XX Hamada K, Nakakido F;
PI
XX WPI; 2001-266212/27.
DR
XX
XX Method for producing male sterile rice and maize by inserting RNase
PT gene and RNase inhibitor genes with promoters into the plant genome -
PT Disclosure; Page 14-17; 29pp; Japanese.
XX
XX The present invention relates to a method for producing male sterile
CC plants. The method comprises inserting a promoter fragment upstream of an
CC RNase gene and a second promoter, upstream of an RNase inhibitor protein
CC gene and inserting it into the plant genome. The method is useful for
CC producing male sterile tobacco, lettuce and rapeseed plants, but
CC preferably rice and maize. The present sequence is a vector used in
CC the method of the present invention.
XX
SQ Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;

Query Match 45.7%; Score 190; DB 22; Length 5228;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 60
Db 5031 ctacggcaatgtaccagctgataataacagttattgaaatttctgaatttaaaactgc 5090

QY 61 atcaataaaawttatgttttctgttgactataataacacctgactgttattttatcaataaa 120
Db 5091 atcaataaaawttatgttttctgttgactataataacacctgactgttattttatcaataaa 5150

QY 121 tatttaaacatattttcttcaagatggggaattaaacatctacaattgcctttcttctatc 180
Db 5151 tatttaaacatattttcttcaagatggggaattaaacatctacaattgcctttcttctatc 5210

QY 181 gaccatgtacatc 192
Db 5211 gaccatgtacatc 5222

RESULT 7
AAZ91097
ID AAZ91097 standard; DNA; 6539 BP.
XX
XX AAZ91097;
XX
DT 06-JUN-2000 (first entry)
```



```
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgaataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 6351 ctacggcaatgtaccagctgaataatcagttattgaaatatttctgaatttaaaacttgc 6410

QY 61 atcaataaaawttatgttttctggactataataacacctgacttgttattttatcaataaa 120
Db 6411 atcaataaaawttatgttttctggactataataacacctgacttgttattttatcaataaa 6470

QY 121 tatttaaacatattttttccaagatgggaataaacaatctacaaaatgccttttcttacc 180
Db 6471 tatttaaacatattttttccaagatgggaataaacaatctacaaaatgccttttcttacc 6530

QY 181 gaccatgtacat 192
Db 6531 gaccatgtacgt 6542

RESULT 9
AAT61394
ID AAT61394 standard; DNA; 6548 BP.
XX AC AAT61394;
XX DT 07-MAY-1997 (first entry)
XX DE Plasmid pTS172.
XX KW Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;
KW niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
KW ribonuclease; RNase; cereal; wheat; Triticum aestivum;
XX plasmid pTS172; ds.
XX OS Chimeric Agrobacterium sp.;
OS Chimeric Oryza sativa;
OS Chimeric cauliflower mosaic virus.
XX FH key Location/Qualifiers
FT 3'UTR complement (2019..2288)
FT /*tag= a
FT /label= 3'nos
FT /note= "3' untranslated region contg. the poly-A
FT signal of Agrobacterium T-DNA nopaline
FT CDS complement (2289..2624)
FT /*tag= b
FT /product= barnase
FT complement (2625..4313)
FT /*tag= c
FT /label= PE1
FT /note= "promoter region of rice El gene"
FT promoter complement (4336..5710)
FT /*tag= d
FT /label= P35S
FT /note= "35S promoter region of cauliflower mosaic
FT virus"
FT CDS 5711..6262
FT /*tag= e
FT /label= Bar
FT /note= "phosphinothricin acetyltransferase"
FT 3'UTR 6243..6496
FT /*tag= f
FT /label= 3'g7
FT /note= "3' untranslated region contg. the poly-A
FT signal of gene 7 of Agrobacterium T-DNA"
XX PN EP757102-A1.
XX PD 05-FEB-1997.
XX PD 04-AUG-1995; 95EP-0401844.
XX PF
```

```
XX 04-AUG-1995; 95EP-0401844.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX PI De Block M;
XX WPI; 1997-111050/11.
XX Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase
XX inhibitor - reduces the cultured cells response to stress and
XX reduces metabolism
XX Example 2; Page 17-20; 25pp; English.
XX Plasmid pTS172 (AAT61394) contains the barnase coding sequence under
CC control of the rice El gene stamen-specific promoter and a
CC phosphinothricin acetyltransferase coding sequence under control of
CC the CaMV 35S promoter. Plasmid pTS172 and plasmid pTS772 (see also
CC AAT61395) were used to transform wheat Spring variety Pavon calli via
CC particle bombardment. Some calli were treated with the poly-(ADP-
CC ribose) polymerase inhibitor niacinamide before, or before and
CC after, bombardment. Healthy, male sterile plants were regenerated
CC only from bombarded calli that were treated with niacinamide. This
CC was believed to be due to more faithful expression characteristics
CC of the integrated stamen-selective barnase gene in these calli
CC and regenerated shoots. For plants transformed with pTS172,
CC foreign DNA was stably incorporated in the wheat genome in 2-3
CC copies.
XX SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 45.7%; Score 190; DB 18; Length 6548;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgaataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 6351 ctacggcaatgtaccagctgaataatcagttattgaaatatttctgaatttaaaacttgc 6410

QY 61 atcaataaaawttatgttttctggactataataacacctgacttgttattttatcaataaa 120
Db 6411 atcaataaaawttatgttttctggactataataacacctgacttgttattttatcaataaa 6470

QY 121 tatttaaacatattttttccaagatgggaataaacaatctacaaaatgccttttcttacc 180
Db 6471 tatttaaacatattttttccaagatgggaataaacaatctacaaaatgccttttcttacc 6530

QY 181 gaccatgtacat 192
Db 6531 gaccatgtacgt 6542

RESULT 10
AAZ91096
ID AAZ91096 standard; DNA; 6548 BP.
XX AC AAZ91096;
XX DT 06-JUN-2000 (first entry)
XX DE E. coli plasmid pTS172 containing synthetic barnase gene.
XX KW Male sterile plant; mutant barnase gene; anther-specific expression;
XX low fidelity PCR; primer; plant breeding; ss.
XX OS Synthetic.
XX PN WO200008176-A1.
XX PD 17-FEB-2000.
XX PF
```

```

PF 03-AUG-1999; 99WO-JP04167.
XX
XX
PR 04-AUG-1998; 99JP-0220060.
XX
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
XX
PI Hamada K, Nakakido F;
XX
XX WPI; 2000-195581/17.
XX
XX
PT Mutate barnase gene for efficient construction of plant transformants,
PT particularly male sterile plants free from any undesirable characters
PT by specifically expressing the gene alone in anther.
XX
XX
PS Example 3; Page 19-23; 30pp; Japanese.
XX
XX
CC The invention relates to the generation of male sterile plants by
CC the introduction of a mutant barnase gene (AAZ91095) for expression
CC specifically in the anther of a plant. This sequence represents the
CC E. coli/Agrobacterium shuttle vector plasmid pRS172 which contains
CC the synthetic barnase gene (AAZ91094) under control of the cauliflower
CC mosaic virus 35S promoter. The vector also contains a region of the
CC Agrobacterium T-DNA gene 7. The vector is used for transmitting the
CC barnase gene to plants via an Agrobacterium tumefaciens host cell.
CC The transformed plant is used in plant breeding.
XX
XX
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 45.7%; Score 190; DB 21; Length 6548;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
Db 6351 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 6410
QY 61 atcaataaaattatgttttctgctgactataataactgactgttatttatcaataaa 120
Db 6411 atcaataaaattatgttttctgctgactataataactgactgttatttatcaataaa 6470
QY 121 tatttaaacatattttcttcaagatgggaattacaatctacaaattgcctttttattc 180
Db 6471 tatttaaacatattttcttcaagatgggaattacaatctacaaattgcctttttattc 6530
QY 181 gaccatgtacat 192
Db 6531 gaccatgtacgt 6542

RESULT 11
AAF86441
ID AAF86441 standard; DNA; 7492 BP.
XX
XX
AC AAF86441;
XX
XX
DT 25-JUN-2001 (first entry)
XX
XX
DE Plasmid pTS346.
XX
XX
KW Male sterile plant; RNAase inhibitor; plasmid pTS346; ds.
XX
XX
OS Unidentified.
XX
XX
PN WO200124616-A1.
XX
XX
PD 12-APR-2001.
XX
XX
PF 12-SEP-2000; 2000WO-JP06222.
XX
XX
PR 30-SEP-1999; 99JP-0279307.
XX
XX
PA (NISR ) JAPAN TOBACCO INC.

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XX
XX
PI Hamada K, Nakakido F;
XX
XX WPI; 2001-266212/27.
XX
XX
PT Method for producing male sterile rice and maize by inserting RNase
PT gene and RNase inhibitor genes with promoters into the plant genome -
XX
XX
PS Disclosure; Page 19-23; 29pp; Japanese.
XX
XX
CC The present invention relates to a method for producing male sterile
CC plants. The method comprises inserting a promoter fragment upstream of an
CC RNase gene and a second promoter, upstream of an RNase inhibitor protein
CC gene and inserting it into the plant genome. The method is useful for
CC producing male sterile tobacco, lettuce and rapeseed plants, but
CC preferably rice and maize. The present sequence is a vector used in
CC the method of the present invention.
XX
XX
SQ Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;

Query Match 45.7%; Score 190; DB 22; Length 7492;
Best Local Similarity 99.0%; Pred. No. 1.5e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 60
Db 7295 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaacttgc 7354
QY 61 atcaataaaattatgttttctgctgactataataactgactgttatttatcaataaa 120
Db 7355 atcaataaaattatgttttctgctgactataataactgactgttatttatcaataaa 7414
QY 121 tatttaaacatattttcttcaagatgggaattacaatctacaaattgcctttttattc 180
Db 7415 tatttaaacatattttcttcaagatgggaattacaatctacaaattgcctttttattc 7474
QY 181 gaccatgtacat 192
Db 7475 gaccatgtacgt 7486

RESULT 12
AAT39337
ID AAT39337 standard; DNA; 1303 BP.
XX
XX
AC AAT39337;
XX
XX
DT 22-JAN-1997 (first entry)
XX
XX
DE Plasmid pTS88 (EcoRI-HindIII fragment).
XX
XX
KW Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
KW transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT misc_feature 1..35
FT /*tag= a
FT /label= pGEM2
FT /note= "polylinker of pGEM2"
FT promoter 36..694
FT /*tag= b
FT /label= P35S
FT /function= 35S promoter of cauliflower mosaic virus
FT CDS 695..967
FT /*tag= c
FT /label= barstar
FT /product= Bacillus amyloliquefaciens barstar
FT polyA_signal 968..1287
FT /*tag= d

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FT	misc_feature	1288..1303	/label= 3'g7 /function= region containing polyadenylation signal of gene 7 og Agrobacterium T-DNA
FT			
FT			
FT			
FT			
FT			
FT			
FT			
XX			
XX	W09626283-A1.		/label= pGEM2 /note= "polylinker of pGEM2"
PN			
XX			
XX	29-AUG-1996.		
XX			
XX	21-FEB-1996;	96WO-EP00722.	
XX			
XX	21-FEB-1995;	95EP-0400364.	
XX			
XX	(PLBZ) PLANT GENETIC SYSTEMS NV.		
PA			
XX	Botterman J, Cornelissen M, Michiels F;		
PI			
XX			
DR	WPI; 1996-402373/40.		
XX			
XX	Prodn. of male sterile plants by transforming with a chimaeric		
PT	construct - comprising a male sterility DNA e.g. barnase and a		
PT	co-regulating gene, e.g. Barstar, into the nuclear genome, useful		
PT	for generating hybrid cultivars		
PT			
XX			
XX	Example 1; Page 38; 56pp; English.		
PS			
XX			
CC	The HindIII-EcoRI fragment (AAT39337) of plasmid pTS98 contains		
CC	used DNA under control of a 35S promoter. The plasmid was		
CC	barstar DNA under control of a 35S promoter. The plasmid was		
CC	used with pTS174 (see also AAT39336) contg. barnase DNA under		
CC	control of the stamen-specific promoter E1 to produce male sterile		
CC	rice cv. Kochihibiki transgenic plants, and with plasmid pVE136		
CC	(see also AAT39338) contg. barnase DNA under control of the stamen-		
CC	specific PCA55 promoter to produce male sterile maize plants.		
CC	Expression of barnase (a ribonuclease) in the stamen leads to male		
CC	sterility. Constitutive expression of barstar counteracts possible		
CC	low level expression of barnase DNA in non-stamen tissue.		
XX			
XX	Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;		
QY	Query Match	45.6%;	Score 189.6; DB 17; Length 1303;
Db	Best Local Similarity	99.5%;	Pred. NO. 1.7e-29;
QY	Matches 189; Conservative	1;	Mismatches 0; Indels 0; Gaps
QY	1	ctacggcaatgtaccagctgatataatcaatcagttattgaaatattctgaattaaacttgc	60
Db	1098		
QY	61	atcaataaawttatgttttcttgacctataataacctgacttgtattttatcaataaa	120
Db	1158		
QY	121	tatttaaacattattctttccaagatgggaattacaatctacaaatgcctttcttctatc	180
Db	1218		
QY	181	gaccatgtac	190
Db	1278		
QY	181	gaccatgtac	1287
Db	1278		
RESULT	13		
AAQ14529			
ID	AAQ14529	standard; DNA; 3201 BP.	
XX			
XX	AAQ14529;		
XX			
DT	27-JAN-1992	(first entry)	
XX			
DE	pPS029	Bt ICP coding sequence.	

```

OS Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT misc_feature 1..25
FT /*tag= a
FT /note= "right border repeat from TL-DNA from pTIB6S3"
FT 26..53
FT /*tag= b
FT /note= "synthetic polylinker derived sequences"
FT 54..90
FT /*tag= c
FT /note= "residual sequence from TL-DNA at right
FT border repeat"
FT 91..97
FT /*tag= d
FT /note= "synthetic polylinker derived sequences"
FT complement (98..309)
FT /*tag= e
FT /note= "3' UTR from TL-DNA gene 7 of pTIB6S3"
FT 310..330
FT /*tag= f
FT /note= "synthetic polylinker derived sequences"
FT complement (331..882)
FT /*tag= g
FT /note= "Streptomyces hygrosopicus bialaphos
FT resistance (bar) gene"
FT complement (883..2608)
FT /*tag= h
FT /note= "atsIA ribulose-1,5-biphosphate carboxylase
FT small subunit gene from Arabidopsis thaliana"
FT 2609..2658
FT /*tag= i
FT /note= "synthetic polylinker derived sequences"
FT complement (2659..2919)
FT /*tag= j
FT /note= "TaqI fragment from 3' UTR of nopaline
FT synthase gene from T-DNA of pRi737 and
FT containing plant polyadenylation signals"
FT 2920..2940
FT /*tag= k
FT /note= "synthetic polylinker derived sequences"
FT 2941..2980
FT /*tag= l
FT /note= "downstream of Bacillus amyloliquefaciens
FT barstar coding region"
FT complement (2981..3253)
FT /*tag= m
FT /note= "Barstar gene coding region from Bacillus
FT amyloliquefaciens"
FT complement (3254..4762)
FT /*tag= n
FT /note= "anther-specific gene TA29 promoter from
FT Nicotiana tabacum"
FT 4763..4807
FT /*tag= o
FT /note= "synthetic polylinker derived sequences"
FT 4808..4832
FT /*tag= p
FT /note= "left border repeat from TL-DNA from pTIB6S3"
FT
XX
PN WO200141558-A1.
XX
PD 14-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-EP12872.
XX
PR 08-DEC-1999; 99US-0457037.
XX
PA (AVET ) AVENTIS CROPS SCIENCE NV.
XX
PI De Both G, De Beuckeleer M;
XX
DR WPI; 2001-381419/40.

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XX Transgenic winter oilseed rape plants suited for producing hybrid seed
FT with improved qualities, comprises a male-sterility gene and fertility
FT restorer gene, integrated into the genome
XX
XX Example 1; Page 80-82; 98pp; English.
XX
CC The specification describes a pair of transgenic winter oilseed rape
CC plants suited for producing hybrid seed. One of the plants has an
CC expression cassette comprising a male-sterility gene, and the other
CC plant has an expression cassette comprising a fertility restorer gene,
CC integrated into the genome. The fertility restorer gene is capable of
CC preventing the activity of the male-sterility gene. The plant pair is
CC useful for producing hybrid seed. Plants developed from the hybrid
CC seed have agronomic performance, genetic stability and adaptability to
CC different genetic backgrounds. The present sequence represents
CC a plasmid pTHW118. This plasmid comprises the barstar gene, which acts as
CC a fertility restorer gene. The plasmid is used to create transgenic
CC plants of the invention.
XX
SQ Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
Query Match 45.6%; Score 189.6; DB 22; Length 4832;
Best Local Similarity 99.5%; Pred. No. 1.8e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatatcaatcagttattgaaatattctgaatttaaacctgc 60
DB 243 CTACGGCAATGTACCAGCTGATATATCATCATGATTATTCGAATTTTGAATTTAACTTGC 184
QY 61 atcaataaawttatgtttttgttggaactataataacctgactgtttatttatcaataa 120
DB 183 ATCAATAAATTTATGTTTGTGCTGGACTATATACCTGACTTGTATTATTATCAATAA 124
QY 121 tattaaacatatattcttccaagtgaggaaattaaacatctacaaattgcctttcttattc 180
DB 123 TATTAAACATATATTCTTCAAGATGGGAATTAAACATCTACAAATTCCTTTCTTATC 64
QY 181 gaccatgtac 190
DB 63 GACCATGTAC 54
RESULT 15
AAT59531/c
ID AAT59531 standard; DNA; 4946 BP.
XX
AC AAT59531;
XX
DT 07-MAY-1997 (first entry)
XX
DE T-DNA of plasmid pTHW107.
XX
KW Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;
KW niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
KW ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus;
KW plasmid pTHW107; ds.
XX
OS Chimeric Agrobacterium sp.;
OS Chimeric Arabidopsis thaliana;
OS Chimeric Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT misc_RNA complement (1..25)
FT /*tag= a
FT /label= RB
FT /note= "T-DNA right border"
FT complement (97..330)
FT /*tag= b
FT /label= 3'g7
FT /note= "3' untranslated region contg. the poly-A
FT signal of gene-7 of Agrobacterium T-DNA"

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Search completed: December 19, 2001, 17:32:10
Job time: 4167 sec

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Query Match      45.6%; Score 189.6; DB 18; Length 4946;
Best Local Similarity 99.5%; Pred. No. 1.8e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacggcaatgtaccagctgataataatcagttattggaatatattctgaattaaacttgc 60
    |||||
Db 243 CTACGGCAATGTACCAGCTGATATATACGTTATTGGAATATTTCTGAATTTAAACTTGC 184
    |||||

OY 61 atcaataaaawttatgtttttgccttggaactataatcacctgacttctatttttatcaataaa 120

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H

RESULT 4
AX063413
LOCUS AX063413 7599 bp DNA PAT 24-JAN-2001
DEFINITION Sequence 5 from Patent WO0100833.
ACCESSION AX063413
VERSION AX063413.1 GI:12541201
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 7599)
AUTHORS Hoffmann,B., Mollner,P. and Pelletier,G.
TITLE Promoter expressed specifically in the cells of plant roots,
recombinant vectors and host cells comprising same and transgenic
plants obtained
JOURNAL Patent: WO 0100833-A 5 04-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)
FEATURES
source Location/Qualifiers
l. .7599
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="ADN-T de PGK85"
BASE COUNT 1972 a 1938 c 1937 g 1752 t
ORIGIN
Query Match 46.3%; Score 192.6; DB 6; Length 7599;
Best Local Similarity 99.5%; Pred. No. 1.3e-24;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 6579 CTACGGCAATGTACCAGCTGATATAATCACTATTGAAATATTCTGAATTTAAACTTGC 6638
QY 61 atcaataaaavttatgttttgcctggactataataacctgactgttattttatcaataaaa 120
Db 6639 ATCAATAAAATTTATGTTTTCCTGGACTATAATACCTGACTTGTATTATCAATAAAA 6698
QY 121 tatttaaacatattttcttcaagatgggaattaaacatcacaaatgcctttcttctatc 180
Db 6699 TATTAAACATATATTTCTTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 6758
QY 181 gaccatgtacatc 193
Db 6759 GACCATGTACATC 6771
RESULT 5
LOCUS E31991 6539 bp DNA PAT 07-FEB-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31991
VERSION E31991.1 GI:13021588
KEYWORDS JP 2000041682-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 6539)
AUTHORS Kazuyuki,H.F.N.N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 4 15-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Escherichia coli LE392
PN JP 2000041682-A/4
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
PR KAZUYUKI HAMADA,FUMIO NAKAKIDO
PI C12N15/09,A01H5/00,C12N5/10,C12N9/22/(C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,(C12N5/00,C12R1:91)
CC

PH Key Location/Qualifiers
FT source l. .6539
/organism="Escherichia coli LE392".
FEATURES
source Location/Qualifiers
l. .6539
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 1755 a 1578 c 1519 g 1687 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6539;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 6342 CTACGGCAATGTACCAGCTGATATAATCACTATTGAAATATTCTGAATTTAAACTTGC 6401
QY 61 atcaataaaavttatgttttgcctggactataataacctgactgttattttatcaataaaa 120
Db 6402 ATCAATAAAATTTATGTTTTCCTGGACTATAATACCTGACTTGTATTATCAATAAAA 6461
QY 121 tatttaaacatattttcttcaagatgggaattaaacatcacaaatgcctttcttctatc 180
Db 6462 TATTAAACATATATTTCTTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 6521
QY 181 gaccatgtacat 192
Db 6522 GACCATGTACGT 6533
RESULT 6
LOCUS A60109 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent WO9706267.
ACCESSION A60109
VERSION A60109.1 GI:3715125
KEYWORDS Plasmid PTS172.
SOURCE Plasmid PTS172.
ORGANISM plasmids.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: WO 9706267-A 2 20-FEB-1997;
PLANT GENETIC SYSTEMS NV (BE)
FEATURES
source Location/Qualifiers
l. .6548
/organism="plasmid PTS172"
/db_xref="taxon:106340"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
Query Match 45.7%; Score 190; DB 6; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 60
Db 6351 CTACGGCAATGTACCAGCTGATATAATCACTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaavttatgttttgcctggactataataacctgactgttattttatcaataaaa 120
Db 6411 ATCAATAAAATTTATGTTTTCCTGGACTATAATACCTGACTTGTATTATCAATAAAA 6470
QY 121 tatttaaacatattttcttcaagatgggaattaaacatcacaaatgcctttcttctatc 180
Db 6471 TATTAAACATATATTTCTTTCAAGATGGGAATTAACATCTACAAATTCCTTTCTTATC 6530
QY 181 gaccatgtacat 192
Db 6533 GACCATGTACGT 6548

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Db 6531 GACCATGTACGT 6542

RESULT 7
A76916 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent EP0757102.
ACCESSION A76916
VERSION A76916.1 GI:6088713
KEYWORDS Plasmid pTS172.
SOURCE Plasmid pTS172.
ORGANISM Plasmids.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De,B.M.
TITLE GENETIC TRANSFORMATION USING A PARP INHIBITOR
JOURNAL Patent: EP 0757102-A 2 05-FEB-1997;
PLANT GENETIC SYSTEMS NW (BE)
FEATURES
    source
        Location/Qualifiers
            /organism="Plasmid pTS172"
            /db_xref="taxon:106340"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
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    Query Match 45.7%; Score 190; DB 6; Length 6548;
    Best Local Similarity 99.0%; Pred. No. 3.6e-24;
    Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaattttaaacttgc 60
Db 6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaawttattgtttcttgcttgactataataactgactgttatttattcaataaa 120
Db 6411 ATCAATAAAATTTATGTTTGTCTTGACTATAATACTGACTTGTATTATTAATAATAA 6470
QY 121 tatttaaaactatattcttctcaagatgggaattacaatctacaaattgcctttcttacc 180
Db 6471 TATTTAAACTATATTCTTTCAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 6530
QY 181 gaccatgtacat 192
Db 6531 GACCATGTACGT 6542

RESULT 9
E31990 6548 bp DNA PAT 07-FEB-2001
DEFINITION Mutated barnase gene and transgenic plant thereof.
ACCESSION E31990
VERSION E31990.1 GI:13021587
KEYWORDS JP 2000041682-A/3.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 6548)
AUTHORS Kazuyuki,H.F.N.N.
TITLE Mutated barnase gene and transgenic plant thereof
JOURNAL Patent: JP 2000041682-A 3 15-FEB-2000;
COMMENT JAPAN TOBACCO INC
OS Escherichia coli LE392
PN JP 2000041682-A/3
PD 15-FEB-2000
PF 04-AUG-1998 JP 19982220060
PR KAZUYUKI HAMADA,FUMIO NAKAKIDO
PC C12N15/09,A01H5/00,C12N5/10,C12N9/22/(C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..6548
    /organism="Escherichia coli LE392".
FEATURES
    source
        Location/Qualifiers
            1..6548
            /organism="unidentified"
            /db_xref="taxon:32644"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
    Query Match 45.7%; Score 190; DB 6; Length 6548;
    Best Local Similarity 99.0%; Pred. No. 3.6e-24;
    Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaattttaaacttgc 60
Db 6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6410
QY 61 atcaataaaawttattgtttcttgcttgactataataactgactgttatttattcaataaa 120
Db 6411 ATCAATAAAATTTATGTTTGTCTTGACTATAATACTGACTTGTATTATTAATAATAA 6470
QY 121 tatttaaaactatattcttctcaagatgggaattacaatctacaaattgcctttcttacc 180
Db 6471 TATTTAAACTATATTCTTTCAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 6530
QY 181 gaccatgtacat 192
Db 6531 GACCATGTACGT 6542

RESULT 8
AR098308 6548 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6074876.
ACCESSION AR098308
VERSION AR098308.1 GI:12807565
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De Block,M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: US 6074876-A 2 13-JUN-2000;
FEATURES
    source
        Location/Qualifiers
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            /organism="unknown"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN
    Query Match 45.7%; Score 190; DB 6; Length 6548;
    Best Local Similarity 99.0%; Pred. No. 3.6e-24;
    Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaattttaaacttgc 60
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RESULT 10
AR078675/c
LOCUS AR078675 7811 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5962768.
ACCESSION AR078675
VERSION AR078675.1 GI:10005421
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7811)
AUTHORS Cornelissen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
TITLE Marker gene
JOURNAL Patent: US 5962768-A 5 05-OCT-1999;
FEATURES
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        Location/Qualifiers
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                /organism="unknown"
BASE COUNT 1950 a 1906 c 1873 g 2082 t
ORIGIN

Query Match 45.7%; Score 190; DB 6; Length 7811;
Best Local Similarity 99.0%; Pred. No. 3.5e-24;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaacttgc 60
    |||||||
Db 629 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCGAATTTAAACTTGC 570

Qy 61 atcaataaawttatgttttctgctggactataataacacgtgactgttattttatcaataaa 120
    |||||||
Db 569 ATCAATAAATTTATGTTTCTGCTGGACTATAATACCTGACTCTGTTTATTATCAATAAAA 510

Qy 121 tatttaacatattctttcaagatgggaattaaacatctacaattgcctttcttctatc 180
    |||||||
Db 509 TATTTAACTATATTCTTTCAAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 450

Qy 181 gaccatgtacat 192
    |||||||
Db 449 GACCATGTACGT 438

Query Match 45.6%; Score 189.6; DB 6; Length 4832;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
I44104
LOCUS I44104 3200 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 23 from patent US 5633446.
ACCESSION I44104
VERSION I44104.1 GI:2469202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3200)
AUTHORS Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.
TITLE Modified Bacillus thuringiensis insecticidal-crystal protein genes and their expression in plant cells
JOURNAL Patent: US 5633446-A 23 27-MAY-1997;
FEATURES
    source
        Location/Qualifiers
            1..3200
                /organism="unknown"
BASE COUNT 880 a 710 c 720 g 885 t
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 3200;
Best Local Similarity 99.5%; Pred. No. 4.5e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaacttgc 60
    |||||||
Db 2952 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTCGAATTTAAACTTGC 3011

Qy 61 atcaataaawttatgttttctgctggactataataacacgtgactgttattttatcaataaa 120
    |||||||

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Db 3012 ATCAATAAATTTATGTTTCTGCTGGACTATAATACCTGACTGTTTATTATTTATCAATAAA 3071
Qy 121 tatttaacatattctttcaagatgggaattaaacatctacaattgcctttcttctatc 180
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Qy 181 gaccatgtac 190
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Db 3132 GACCATGTAC 3141

RESULT 12
AX172441/c
LOCUS AX172441 4832 bp DNA PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141558.
ACCESSION AX172441
VERSION AX172441.1 GI:14597553
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 4832)
AUTHORS de Both,G. and de Beuckeleer,M.
TITLE Hybrid winter oilseed rape and methods for producing same
JOURNAL Patent: WO 0141558-A 2 14-JUN-2001;
FEATURES
    Location/Qualifiers
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            1..4832
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                /note="T-DNA of plasmid pTHW118"
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            1883..4065
                /note="HpaI restriction fragment"
BASE COUNT 1528 a 883 c 932 g 1488 t
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaacttgc 60
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Qy 61 atcaataaawttatgttttctgctggactataataacacgtgactgttattttatcaataaa 120
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Qy 121 tatttaacatattctttcaagatgggaattaaacatctacaattgcctttcttctatc 180
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Qy 181 gaccatgtac 190
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Db 63 GACCATGTAC 54

RESULT 13
A60108/c
LOCUS A60108 4946 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9706267.
ACCESSION A60108
VERSION A60108.1 GI:3715124
KEYWORDS
SOURCE Transformation vector pTHW107.
ORGANISM Transformation vector pTHW107.
REFERENCE 1 (bases 1 to 4946)
AUTHORS De,B.N.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: WO 9706267-A 1 20-FEB-1997;

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PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
1. .4946
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/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
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Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttcttgctggactataataacctgactgttatttatacaataaa 120
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QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54

RESULT 14
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LOCUS A76915 4946 bp DNA PAT 19-OCT-1999
DEFINITION Sequence 1 from Patent EP0757102.
ACCESSION A76915
VERSION A76915.1 GI:6088712
KEYWORDS Transformation vector pTHW107.
SOURCE Transformation vector pTHW107.
ORGANISM Transformation vector pTHW107.
ARTIFICIAL SEQUENCE; VECTORS.
REFERENCE 1 (bases 1 to 4946)
AUTHORS De B.M.
TITLE GENETIC TRANSFORMATION USING A PARP INHIBITOR
JOURNAL Patent: EP 0757102-A 1 05-FEB-1997;
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Location/Qualifiers
1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatatcaatcagttattgaaattcttgaatttaaaacttgc 60
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QY 121 tatttaaacatattcttctcaagatgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACTATCAATCTACAAATGGCTTTCTTATC 64
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Db 63 GACCATGTAC 54

PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
1. .4946
/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
BASE COUNT 1569 a 891 c 963 g 1523 t
PAT 14-FEB-2001
ORIGIN

Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatatcaatcagttattgaaattcttgaatttaaaacttgc 60
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QY 61 atcaataaawttatgttttcttgctggactataataacctgactgttatttatacaataaa 120
Db 183 ATCAATAAATTTATGTTTCTGGACTATAATACCTGACTTGTATTATTATCAATAAAA 124
QY 121 tatttaaacatattcttctcaagatgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACTATCAATCTACAAATGGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54
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RESULT 15
AR098307/c
LOCUS AR098307 4946 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6074876.
ACCESSION AR098307
VERSION AR098307.1 GI:12807564
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4946)
AUTHORS De Block, M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: US 6074876-A 1 13-JUN-2000;
FEATURES Location/Qualifiers
source 1. .4946
BASE COUNT 1569 a 891 c 963 g 1523 t
ORIGIN
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Query Match 45.6%; Score 189.6; DB 6; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatatcaatcagttattgaaattcttgaatttaaaacttgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 184
QY 61 atcaataaawttatgttttcttgctggactataataacctgactgttatttatacaataaa 120
Db 183 ATCAATAAATTTATGTTTCTGGACTATAATACCTGACTTGTATTATTATCAATAAAA 124
QY 121 tatttaaacatattcttctcaagatgggaattaaacatctacaaattgcctttcttattc 180
Db 123 TATTTAAACTATATTTCTTCAAGATGGGAATTAACTATCAATCTACAAATGGCTTTCTTATC 64
QY 181 gaccatgtac 190
Db 63 GACCATGTAC 54
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Search completed: December 19, 2001, 17:28:06
Job time: 3928 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:33:57 ; Search time 110.23 Seconds
(without alignments)
854.711 Million cell updates/sec

Title: US-09-698-903b-10
Perfect score: 416
Sequence: 1 ctacggcaatgtaccagctg.....catgaacaccacaactcgat 416

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192.6	46.3	5864	3	US-08-894-440-4
2	190	45.7	6548	3	US-08-894-440-1
3	190	45.7	7811	2	US-08-817-188-2
4	189.6	45.6	1303	3	US-08-549-680A-5
5	189.6	45.6	3200	1	US-08-894-440-2
6	189.6	45.6	3200	1	US-08-453-104-23
7	189.6	45.6	3200	1	US-08-694-824-23
8	189.6	45.6	4946	3	US-08-817-188-1
9	189.6	45.6	5560	3	US-08-817-188-5
10	189.6	45.6	7566	2	US-08-232-016-23
11	189.6	45.6	7639	2	US-08-232-016-22
12	188	45.2	5864	3	US-08-894-440-4
13	176.6	42.5	3201	2	US-08-453-104-22
14	176.6	42.5	3201	2	US-08-694-824-22
15	152.8	36.7	1186	1	US-08-064-121-2
16	152.6	36.7	1186	1	US-08-478-015-2
17	152.6	36.7	1186	3	US-08-475-375-2
18	152.6	36.7	1186	3	US-09-084-889-2
19	145.6	35.0	3153	4	US-09-080-625-3
20	145.6	35.0	3336	4	US-09-080-625-2
21	145.6	35.0	3694	4	US-09-080-625-5
22	145.6	35.0	3877	4	US-09-080-625-4
23	142.6	34.3	24595	6	US-08-817-188-1
24	51.2	12.3	80246	4	US-09-078-294-4
25	50.4	12.1	80595	4	US-09-078-294-3
26	41.8	10.0	19124	2	US-08-487-826B-13
27	41.4	10.0	15397	2	US-08-673-768-1

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c 31 40.2 9.7 289 4 US-09-007-005-17
c 32 40.2 9.7 289 4 US-09-244-796-17
c 33 40 9.6 1588 3 US-09-058-489-45
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c 35 39 9.4 9048 3 US-08-973-273-4
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c 37 38.6 9.3 3947 4 US-08-975-762-47
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c 42 37.6 9.0 1056 3 US-08-995-654-1
c 43 37.4 9.0 8654 1 US-08-920-812-6
c 44 37.4 9.0 8654 1 US-08-920-827-6
c 45 37.4 9.0 8654 1 US-08-921-177-6

ALIGNMENTS

RESULT 1
US-08-894-440-4
; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTColl3
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of nopaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
; US-08-894-440-4

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Best Local Similarity 99.5%; Pred. No. 1.4e-35;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 121 tatttaaacataattttcttccaagatgggaattacaatactacaattgcctttcttacc 180
Db 5740 tatttaaacataattttcttccaagatgggaattacaatactacaattgcctttcttacc 5799
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; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NM50R
; CURRENT APPLICATION NUMBER: US/08/894,440
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
; NAME/KEY: misc_feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2283)..(2289))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
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; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific EI gene of rice
; OTHER INFORMATION: (PEI)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal to gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; US-08-894-440-1
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Best Local Similarity 99.0%; Pred. No. 5.7e-35;
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QY 121 tatttaaacataattttcttccaagatgggaattacaatactacaattgcctttcttacc 180
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QY 181 gaccatgtacat 192
Db 6531 gaccatgtacat 6542
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RESULT 3
US-08-817-188-2
; Sequence 2, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS172
; NAME/KEY: misc_feature
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US-08-894-440-2

; Sequence 2, Application US/08894440
; Patent No. 6025546

; GENERAL INFORMATION:

; APPLICANT: PLANT GENETIC SYSTEMS N.V.

; TITLE OF INVENTION: Method to obtain male sterile plants

; FILE REFERENCE: NMSCOR

; CURRENT APPLICATION NUMBER: US/08/894,440

; CURRENT FILING DATE: 1997-11-12

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1303

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HindIII-EcORI

; OTHER INFORMATION: fragment of pRS8

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(35)

; OTHER INFORMATION: polylinker of pGEM2 (pGEM2)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (36)..(694)

; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain

; OTHER INFORMATION: CM1841 (P35S)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (695)..(967)

; OTHER INFORMATION: region coding for barstar of Bacillus

; OTHER INFORMATION: amyloliquefaciens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (968)..(1287)

; OTHER INFORMATION: region containing polyadenylation signal of gene 7

; OTHER INFORMATION: Of Agrobacterium T-DNA (3'g7)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1288)..(1303)

; OTHER INFORMATION: polylinker of pGEM2

US-08-894-440-2

Query Match 45.6%; Score 189.6; DB 3; Length 1303;

Best Local Similarity 99.5%; Pred. No. 6e-35;

Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttatgaaatattctgaaatttaaaacttgc 60

Db 1098 ctacggcaatgtaccagctgataataatcagttatgaaatattctgaaatttaaaacttgc 1157

QY 61 atcaataaaawttatgtttttgttggtgactataataacccgactgtttattttatcaataaa 120

Db 1158 atcaataaaawttatgtttttgttggtgactataataacccgactgtttattttatcaataaa 1217

QY 121 tatttaaacctattcttctcaagatgggaataacacatcacaattgcctttttatc 180

Db 1218 tatttaaacctattcttctcaagatgggaataacacatcacaattgcctttttatc 1277

QY 181 gaccatgtac 190

Db 1278 gaccatgtac 1287

RESULT 6

US-08-453-104-23

; Sequence 23, Application US/08453104

; Patent No. 5633446

; GENERAL INFORMATION:

; APPLICANT: CORNELISSEN, Marc

; APPLICANT: SOETAERT, Piet

; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."

Query Match 45.6%; Score 189.6; DB 1; Length 3200;

Best Local Similarity 99.5%; Pred. No. 6.5e-35;

Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttatgaaatattctgaaatttaaaacttgc 60

Db 2952 ctacggcaatgtaccagctgataataatcagttatgaaatattctgaaatttaaaacttgc 3011

QY 61 atcaataaaawttatgtttttgttggtgactataataacccgactgtttattttatcaataaa 120

Db 3012 ATCAATAAAATTTATGTTTTCCTGGGACTATAATACCTGACTGTTTATTTATCAATAAA 3071

QY 121 tatttaaacctattcttctcaagatgggaataacacatcacaattgcctttttatc 180

Db 3072 TATTTAAACTATATTCTTTTCAAGATGGGAATTAACATCTACAAATTCCTTTTCTTATC 3131

QY 181 gaccatgtac 190

Db 3132 GACCATGTAC 3141

RESULT 7

US-08-694-824-23

; Sequence 23, Application US/08694824

; Patent No. 5877306

GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETART, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22131-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30.427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2078..2082
OTHER INFORMATION: /note= "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
US-08-694-824-23

Query Match 45.6%; Score 189.6; DB 2; Length 3200;
Best Local Similarity 99.5%; Pred. No. 6.5e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaactgc 60
Db 2952 CTACGGCAATGTACCAGCTGATATATCAGTATTGAATATTTCTGAAATTTAAACTTGC 3011
QY 61 atcaataaaatgtatgttttgcctggactataataactgactgttattttatcaataaa 120
Db 3012 ATCAATAAATTTATGTTTGTCTGGACTATATACCTGACTTGTATTATTTATCAATAAA 3071
QY 121 tatttaaacatatttcttccaagatgggaattacaatctacaataatgcctttcttctatc 180
Db 3072 TATTAAACATATATTTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTCTTATC 3131
QY 181 gaccatgtac 190
Db 3132 GACCATGTAC 3141

RESULT 8
US-08-817-188-1/c
Sequence 1, Application US/08817188
Patent No. 6074876
GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4946
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
OTHER INFORMATION: plasmid pTHW107
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3' g7: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((4922)..(4946))
OTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1

Query Match 45.6%; Score 189.6; DB 3; Length 4946;
Best Local Similarity 99.5%; Pred. No. 6.8e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaaatttaaaactgc 60
Db 243 CTACGGCAATGTACCAGCTGATATATCAGTATTGAATATTTCTGAAATTTAAACTTGC 184

QY 61 atcaataaawttatgtttttgttgactataataacctgactgtttattttatcaataaa 120
 Db 183 ATCAATAAATTTATGTTTGTGCTGACTATAATACCTGACTGTATTATCAATAAAA 124
 QY 121 tatttaaacattattctttccaagatgggaattacacattacataaattgcctttcttacc 180
 Db 123 TATTAAACTATATTCTTTCAAGATGGGAATTACATCTACAAATTCCTTTCTTATC 64
 QY 181 gaccatgtac 190
 Db 63 GACCATGTAC 54

RESULT 9

US-08-817-188-5/c
 ; Sequence 5, Application US/08817188
 ; Patent No. 6074876
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BLOCK, MARC
 ; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
 ; FILE REFERENCE: 2121-0127P
 ; CURRENT APPLICATION NUMBER: US/08/817,188
 ; CURRENT FILING DATE: 1997-05-15
 ; EARLIER APPLICATION NUMBER: PCT/EP96/03366
 ; EARLIER FILING DATE: 1996-07-31
 ; EARLIER APPLICATION NUMBER: EP 95401844.6
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 5560
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
 ; OTHER INFORMATION: plasmid pTHW142
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(25)
 ; OTHER INFORMATION: RB: right border sequence of octopline TL-DNA from
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (84)..(296)
 ; OTHER INFORMATION: 3' g7: 3' untranslated region containing the
 ; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (318)..(869)
 ; OTHER INFORMATION: bar: region coding for phosphinotricin
 ; OTHER INFORMATION: acetyltransferase
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (830)..(2760)
 ; OTHER INFORMATION: PSSU: promoter region of Rubisco small subunit
 ; OTHER INFORMATION: gene of Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (2765)..(3058)
 ; OTHER INFORMATION: 3' untranslated region of the CamV 35S transcript
 ; OTHER INFORMATION: containing polyadenylation signals
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (3059)..(5056)
 ; OTHER INFORMATION: uidA: region coding for beta-glucuronidase
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (4483)..(4671)
 ; OTHER INFORMATION: IV2: region corresponding to the second intron of
 ; OTHER INFORMATION: the ST-LS1 gene
 ; FEATURE:
 ; NAME/KEY: misc_feature

; LOCATION: (5067)..(5502)
 ; OTHER INFORMATION: P35S: 35S promoter region of CamV
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5533)..(5560)
 ; OTHER INFORMATION: LB: left border sequence of octopline TL-DNA from
 ; OTHER INFORMATION: pT186S3
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5058)..(5059)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5077)..(5078)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5476)..(5479)
 ; OTHER INFORMATION: region with unknown sequence (may contain up to 20
 ; OTHER INFORMATION: nucleotides)
 ; US-08-817-188-5

Query Match 45.6%; Score 189.6; DB 3; Length 5560;
 Best Local Similarity 99.5%; Pred. No. 6.9e-35;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataacagttattgaaatattctgaatttaaaacttgc 60
 Db 230 CTACGGCAATGTACCAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 171
 QY 61 atcaataaawttatgtttttgttgactataataacctgactgtttattttatcaataaa 120
 Db 170 ATCAATAAATTTATGTTTGTGCTGACTATAATAACCTGACTGTGTTATTTATCAATAAA 111
 QY 121 tatttaaacattattctttccaagatgggaattacacattacataaattgcctttcttacc 180
 Db 110 TATTAAACTATATTCTTTCAAGATGGGAATTACATCTACAAATTCCTTTCTTATC 51
 QY 181 gaccatgtac 190
 Db 50 GACCATGTAC 41

RESULT 10

US-08-232-016-23
 ; Sequence 23, Application US/08232016
 ; Patent No. 5952547
 ; GENERAL INFORMATION:
 ; APPLICANT: CORNELISSEN, Marc
 ; APPLICANT: SOETABERT, Piet
 ; APPLICANT: STAM, Maïke
 ; APPLICANT: DOCKX, Jan
 ; APPLICANT: VAN AARSEN, Roel
 ; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
 ; NUMBER OF INVENTION: PLANT CELLS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,016

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; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid DNA designated as pPS0212
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1785
; OTHER INFORMATION: /note= "Coding region of a
; OTHER INFORMATION: truncated modified bt2 (cryIAB) gene, also designated as the
; OTHER INFORMATION: cryIAB6 gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1793..2026
; OTHER INFORMATION: /note= "3' regulatory sequence
; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
; OTHER INFORMATION: T-DNA gene 7."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2396..2921
; OTHER INFORMATION: /note= "35S promoter sequence
; OTHER INFORMATION: derived from Cauliflower mosaic virus."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2922..3581
; OTHER INFORMATION: /note= "Coding sequence of
; OTHER INFORMATION: chloramphenicol acetyl transferase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3582..4407
; OTHER INFORMATION: /note= "3' regulatory sequence
; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
; OTHER INFORMATION: T-DNA octopine synthase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5600..6457
; OTHER INFORMATION: /note= "Sequence complementary to
; OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7071..7566
; OTHER INFORMATION: /note= "TR1' and TR2 promoter
; OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
; OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
; US-08-232-016-23
;
; Query Match 45.6%; Score 189.6; DB 2; Length 7566;
; Best Local Similarity 99.5%; Pred. No. 7.1e-35;
; Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; 1 ctacggcaatgtaccagctgataataatcagttatttgaataatttctgaatttaacttgc 60
; |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1881 CTACGGCAATGTACCAGCTGATATAATCATCAGTTATTGAATATTCTGAATTTAAACTTGC 1940
QY 61 atcaataaawttatgttttctgctggactataatacacctgactgtgtttattttatcaataaa 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1941 ATCAATAAATTTATGTATTTTCTGGACTATAATACCTGACTTGTATTTTATCAATAAA 2000
QY 121 tatttaaacatatttttcaagatgggaattaaacatctacaaatgacctttcttctatc 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2001 TATTAAACATATATTCTTCAAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 2060
QY 181 gaccatgtac 190
|||||:|||||
Db 2061 GACCATGTAC 2070

RESULT 11
US-08-232-016-22
; Sequence 22, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid DNA designated as pJD884
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1869
; OTHER INFORMATION: /note= "Coding region of a
; OTHER INFORMATION: truncated bt2 (cryIAB) gene, also designated as the bt884
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: 1877..2110
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA gene 7."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2480..3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3006..3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3666..4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7155..7639
OTHER INFORMATION: /note= "TR1' and TR2' promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA."
US-08-232-016-22
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Query Match 45.6%; Score 189.6; DB 2; Length 7639;
Best Local Similarity 99.5%; Pred. No. 7.1e-35;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaacctgc 60
Db 1965 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 2024

QY 61 atcaataaawttatgttttctgctggactataataactgactgttattttatcaataaa 120
Db 2025 ATCAATAAATTTATGTTTCTGCTGGACATATAATCAGTTGTTTAAATTTAACTTGC 2084

QY 121 tatttaaacctattctttcgaagatggaataaacatcacaaatgcctttcttattc 180
Db 2085 TATTTAACATATATTCTTTCAAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 2144

QY 181 gaccatgtac 190
Db 2145 GACCATGTAC 2154
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```
RESULT 12
US-08-894-440-4/c
Sequence 4, Application US/08894440
Patent No. 6025546
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 5864
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
```

```
OTHER INFORMATION: plasmid pTCO113
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (pssu)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: Agrobacterium T-DNA (Phos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4
```

```
Query Match 45.2%; Score 188; DB 3; Length 5864;
Best Local Similarity 98.9%; Pred. No. 1.6e-34;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgataataatcagttattgaaatattctgaatttaaacctgc 60
Db 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAACTTGC 184

QY 61 atcaataaawttatgttttctgctggactataataactgactgttattttatcaataaa 120
Db 183 ATCAATAAATTTATGTTTCTGCTGGACATATAATCAGTTGTTTAAATTTAACTTGC 124

QY 121 tatttaaacctattctttcgaagatggaataaacatcacaaatgcctttcttattc 180
Db 123 TATTTAACATATATTCTTTCAAGATGGGAATTAACATCTACAAATTCGCTTTTCTTATC 64
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Qy 181 gaccatgtac 190
|||||
Db 63 GACCATGTAC 54

RESULT 13

US-08-453-104-22

; Sequence 22, Application US/08453104

; Patent No. 5633446

; GENERAL INFORMATION:

; APPLICANT: CORNELISSEN, Marc

; APPLICANT: SOETAERT, Piet

; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan

; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS

; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

; TITLE OF INVENTION: IN PLANT CELLS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/453,104

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,869

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: GB 90401055.0

; FILING DATE: 18-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa S

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 010830-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2151..2155

; OTHER INFORMATION: /note= "Nucleotides 2151-2155

; OTHER INFORMATION: wherein N is not known."

US-08-453-104-22

Query Match 42.5%; Score 176.6; DB 1; Length 3201;
Best Local Similarity 99.4%; Pred. No. 5.7e-32;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaatttaaaccttgc 60
|||||
Db 3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 3084

Qy 61 atcaataaaawttatgttttctgtggactataataacacctgacttattttatcaataaa 120
|||||
Db 3085 ATCAATAAAATTTATGTTTTTCTGTTGGACTATAATAACCTGACTTGTATTATTTATCAATAAA 3144

Qy 121 tatttaaacatatatttcttcaagatgggaattaacatctctacaatgcctttctt 177
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Db 3145 TATTTAAACTATATTCTTTCAGATGGGAATTAAACATCTACAAATTCGCCTTTCTT 3201

RESULT 14

US-08-694-824-22

; Sequence 22, Application US/08694824

; Patent No. 5877306

; GENERAL INFORMATION:

; APPLICANT: CORNELISSEN, Marc

; APPLICANT: SOETAERT, Piet

; APPLICANT: STAM, Maïke

; APPLICANT: DOCKX, Jan

; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS

; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

; TITLE OF INVENTION: IN PLANT CELLS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/694,824

; FILING DATE: 09-AUG-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,869

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: GB 90401055.0

; FILING DATE: 18-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa S

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 010830-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2151..2155

; OTHER INFORMATION: /note= "Nucleotides 2151-2155

; OTHER INFORMATION: wherein N is not known."

US-08-694-824-22

Query Match 42.5%; Score 176.6; DB 2; Length 3201;
Best Local Similarity 99.4%; Pred. No. 5.7e-32;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgataataatcagttattgaaatatttctgaatttaaaccttgc 60
|||||
Db 3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 3084

Qy 61 atcaataaaawttatgttttctgtggactataataacacctgacttattttatcaataaa 120
|||||
Db 3085 ATCAATAAAATTTATGTTTTTCTGTTGGACTATAATAACCTGACTTGTATTATTTATCAATAAA 3144

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QY 121 tatttaaacatatttttcaagatggggaattacaacatctacaaattgcctttctt 177
|||||
Db 3145 TATTAAACTATATTCTTCAAGATGGGAATTAAACATCTACAAATGGCTTTCTT 3201

RESULT 15
US-08-064-121-2
; Sequence 2, Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; NUMBER OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: probe
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..8
; OTHER INFORMATION: /note= "sequence derived from
; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 9..790
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 791..1186
; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
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; OTHER INFORMATION: T-DNA gene 7"
US-08-064-121-2
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Query Match 36.7%; Score 152.6; DB 1; Length 1186;
Best Local Similarity 99.3%; Pred. No. 1.4e-26;
Matches 152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctgatataatcaatcatttgaataatttctgaatttaaaattgc 60
|||||
Db 1033 CTACGGCAATGTACCAGCTGATATATCACTATTGAAATATTCTGAAATTTAAACTTGC 1092

QY 61 atcaataaawttatgttttctgctggactataataacctgactgtttattttatcaataaa 120
|||||
Db 1093 ATCAATAAATTTATGTTTCTGCTTGGACTATATACTGACTTGTATTATTATCAATAAA 1152

QY 121 tatttaaacatatttttcttcaagatggggaatt 153
|||||
Db 1153 TATTAAACTATATTCTTCTTCAAGATGGGAATT 1185
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Search completed: December 19, 2001, 17:34:14
Job time: 4291 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 16:22:38 ; Search time 2253.73 seconds
(without alignments)
95.360 Million cell updates/sec

Title: US-09-698-903b-7

Perfect score: 20
Sequence: 1 ctacggcaatgaccagctg 20

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	em_estfun:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estom:*
5:	em_estpl:*
6:	em_estba:*
7:	em_estro:*
8:	em_estov:*
9:	em_hic:*
10:	gb_est1:*
11:	gb_est2:*
12:	gb_hic:*
13:	gb_gss:*
14:	em_gss_fun:*
15:	em_gss_hum:*
16:	em_gss_inv:*
17:	em_gss_pln:*
18:	em_gss_pro:*
19:	em_gss_rod:*
20:	em_gss_vrt:*
21:	em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	568	11	BI174209
C 2	16.8	84.0	212	10	AA090232
C 3	16.8	84.0	922	11	CG563856
C 4	16.4	82.0	700	13	AQ256131
C 5	16	80.0	170	10	AW370342
C 6	16	80.0	618	10	BE150747
C 7	15.8	79.0	325	11	BF589714
C 8	15.8	79.0	390	10	AI562674
C 9	15.8	79.0	418	11	BE857550
C 10	15.8	79.0	433	11	H66110
C 11	15.8	79.0	433	13	AQ438334
C 12	15.8	79.0	438	11	H66097

RESULT 1

BI174209/c

LOCUS

DEFINITION

OSTF013F8_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to

C46F11.2, mRNA sequence.

BI174209

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

BI174209 568 bp mRNA EST 09-JUL-2001
OSTF013F8_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to
C46F11.2, mRNA sequence.

BI174209

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

ALIGNMENTS

AV632594 AV632594
BF009521 ss91h03.Y
AZ215252 Sheared D
BE508621 dcl8h03.X
BG711246 p91ln.pk0
BF917369 IL3-UT011
AQ948016 Sheared D
AZ187379 SP_1009_A
AQ946406 Sheared D
BF527305 602039373
AL438079 Clone BA0
EG290991 602386981
BF311402 601896616
AW425779 58291 MAR
BB464829 BB464829
AA466153 v973g05.X
C26971 C26971 Rice
AV181598 AV181598
AI880854 att17b03.X
AV193861 AV193861
AW048935 UI-M-BH1-
AU068795 AU068795
AI669082 wb84b08.X
AI835705 UI-M-AI0-
AA478333 zu45b04.X
AI275018 q166h07.X
BE859284 UI-M-AI0-
AV670633 AV670633
AA124200 mg21b05.X
AW341379 x299d05.X
BB283443 BB283443
AI916284 w629a10.X
AI976324 EST270918

15.8 79.0 454 10 AV632594
15.8 79.0 472 11 BF009521
15.8 79.0 602 13 AZ215252
15.8 79.0 622 10 BE508621
15.8 79.0 681 11 BG711246
15.8 79.0 688 11 BF917369
15.8 79.0 711 13 AQ948016
15.8 79.0 712 13 AZ187379
15.8 79.0 731 13 AQ946406
15.8 79.0 923 11 BF527305
15.8 79.0 1009 13 CNS073X5
15.8 79.0 1012 11 EG290991
15.8 79.0 1700 11 BF311402
15.4 77.0 255 10 AW425779
15.4 77.0 277 10 BB464829
15.4 77.0 279 10 AA466153
15.4 77.0 299 11 C26971
15.4 77.0 300 10 AV181598
15.4 77.0 306 10 AI880854
15.4 77.0 375 10 AV193861
15.4 77.0 385 10 AW048935
15.4 77.0 408 10 AU068795
15.4 77.0 422 10 AI669082
15.4 77.0 441 10 AI835705
15.4 77.0 446 10 AA478333
15.4 77.0 447 10 AI275018
15.4 77.0 452 11 BE859284
15.4 77.0 484 10 AV670633
15.4 77.0 508 10 AA124200
15.4 77.0 509 10 AW341379
15.4 77.0 519 10 BB283443
15.4 77.0 526 10 AI916284
15.4 77.0 527 10 AI976324

FEATURES
source Location/Qualifiers
1. .568

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitt, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F., Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M. Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in *C. elegans*
Nat. Genet. 27 (3), 332-336 (2001)
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFsome cloning project : Contact jerome_reboul@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu
POLYA-No.

/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wmcdna"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wmcdna library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

BASE COUNT 146 a 116 c 159 g 147 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 11; Length 568;
Best Local Similarity 94.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ctacggcaatgtaccagct 19
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Db 563 CTACGGCAATATACAGCT 545

RESULT 2
AA090232 212 bp mRNA EST 24-OCT-1996
LOCUS chp0019.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
DEFINITION cDNA 5', mRNA sequence.
ACCESSION AA090232
VERSION AA090232.1 GI:1636716
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 212)
Liew.C.C.
CDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: liewcc@utcc.utoronto.ca

PCR PRIMERS
FORWARD: 5' GCCAAGCTCGAATTAACCTCACTAAAGG 3'
BACKWARD: 5' CCAGTGAATTAATACGACTCACTATAGGCG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.
FEATURES
Location/Qualifiers
1..212
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

BASE COUNT 65 a 53 c 46 g 47 t
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 212;
Best Local Similarity 90.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ctacggcaatgtaccagctg 20

RESULT 3
BG563856 922 bp mRNA EST 10-APR-2001
LOCUS 602584663F1 NIH_MGC_76 Homo sapiens cDNA Clone IMAGE:4712630 5',
DEFINITION mRNA sequence.
ACCESSION BG563856
VERSION BG563856.1 GI:13571508
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 922)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1554 row: m column: 15
High quality sequence stop: 321.
Location/Qualifiers
1..922
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattatgcc); Site_2: SfiI (ggccattatgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGAGCGCGGCGAGATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 243 a 207 c 248 g 224 t
ORIGIN
Query Match 84.0%; Score 16.8; DB 11; Length 922;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ctacggcaatgtaccagctg 20
||||| ||||| ||||| |||||
Db 116 CTCCGGCAATGTACCATCTG 135

RESULT 4
AQ256131/c 700 bp DNA GSS 23-OCT-1998
LOCUS nbxb0015D03r CUGI Rice BAC Library Oryza sativa genomic clone
DEFINITION nbxb0015D03r, DNA sequence.
ACCESSION AQ256131
VERSION AQ256131.1 GI:3780613
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

REFERENCE
AUTHORS      Ehrhartoideae; Oryzeae; Oryza.
TITLE        1. (bases 1 to 700)
JOURNAL      Wing,R.A. and Dean,R.A.
COMMENT      A BAC End Sequencing Framework to Sequence the Rice Genome
              Unpublished (1998)
              Contact: Wing RA
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Tel: 864 656 7288
              Fax: 864 656 4293
              Email: rwing@clemson.edu
              Seq primer: GGAACAGCTATGACCATG
              Class: BAC ends
              High quality sequence stop: 152.

FEATURES
source
1. .700
   /organism="Oryza sativa"
   /strain="Japonica"
   /cultivar="Nipponbare"
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   /clone="nbxb0015D03r"
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   /tissue_type="Leaf"
   /lab_host="E. coli DH10B"
   /note="Vector: pBelosBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
BASE COUNT  130 a  184 c  188 g  198 t
ORIGIN

Query Match      82.0%; Score 16.4; DB 13; Length 700;
Best Local Similarity 94.4%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  acggcaatgtaccagctg 20
      ||||| ||||| |||||
Db  263  ACGCAATGTCCAGCTG 246

RESULT  5
LOCUS    AW370342      170 bp      mRNA      EST      04-FEB-2000
DEFINITION  RC1-BT0255-181099-012-f06 BT0255 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW370342
VERSION    AW370342.1 GI:6874996
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 170)
            HCCP http://www.ludwig.org.br/ORESTES.
REFERENCE  1
AUTHORS    The FAPESP/LICR Human Cancer Genome Project
TITLE      Unpublished (1999)
JOURNAL    Contact: Simpson A.J.G.
COMMENT

Ehrhartoideae; Oryzeae; Oryza.
1. (bases 1 to 700)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 152.

FEATURES
source
1. .700
   /organism="Oryza sativa"
   /strain="Japonica"
   /cultivar="Nipponbare"
   /db_xref="taxon:4530"
   /clone="nbxb0015D03r"
   /clone_lib="CUGI Rice BAC Library"
   /tissue_type="Leaf"
   /lab_host="E. coli DH10B"
   /note="Vector: pBelosBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
BASE COUNT  130 a  184 c  188 g  198 t
ORIGIN

Query Match      82.0%; Score 16; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  cggcaatgtaccagct 19
      ||||| ||||| |||||
Db  140  CGGCAATGTACCAGCT 155

RESULT  6
LOCUS    BE150747      618 bp      mRNA      EST      21-JUN-2000
DEFINITION  RC1-HT0269-010300-014-h02 HT0269 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE150747
VERSION    BE150747.1 GI:8613377
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 618)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC1-HT0269-010
            300-014-h02st3=2000-03-01st4=1)

```

```

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1st2-RC1-BT0255-
181099-012-f06st3=1999-10-18st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 170.

FEATURES
source
1. .170
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone_lib="BT0255"
   /dev_stage="Adult"
   /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT  37 a  40 c  60 g  33 t
ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  cggcaatgtaccagct 19
      ||||| ||||| |||||
Db  140  CGGCAATGTACCAGCT 155

RESULT  6
LOCUS    BE150747      618 bp      mRNA      EST      21-JUN-2000
DEFINITION  RC1-HT0269-010300-014-h02 HT0269 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE150747
VERSION    BE150747.1 GI:8613377
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 618)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC1-HT0269-010
            300-014-h02st3=2000-03-01st4=1)

```

Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 617.
Location/Qualifiers
1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0269"
/dev_stage="Adult"
/note="Organ: head/neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSRES PCR (O.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
227 a 121 c 106 g 164 t

FEATURES

source

BASE COUNT
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ggcaatgtaccagctg 20
|||||
Db 33 GGCAATGTACCAGCTG 48

RESULT 7
BF589714/c
LOCUS
DEFINITION
nao08h06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254267 3'
similar to TR:Q99829 Q99829 COPINE 1.; mRNA sequence.
BF589714
VERSION
KEYWORDS
SOURCE
ORGANISM

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 325)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: 400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 325

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3254267"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization

FEATURES

source

reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 110192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT 84 a 84 c 91 g 66 t
ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 325;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 tacggcaatgtaccagctg 20
|||||
Db 245 TAAGGCAATGTAACAGCTG 227

RESULT 8
AI562674
LOCUS
DEFINITION
TENS2662 T. cruzi epimastigote normalized cDNA Library Trypanosoma
cruzi cDNA clone 2662 5', mRNA sequence.
AI562674
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Trypanosoma cruzi.
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 390)
Verdun,R.E., Di Paolo,N.C., Urmenyi,T.P., Rondinelli,E., Frasch
,A.C.C. and Sanchez,D.O.
Gene discovery through expressed sequence tag sequencing in
Trypanosoma cruzi
Infect. Immun. 66 (11), 5393-5398 (1998)
99003155
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz entre Albarillos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS, Argentina
Tel: (54-1)752-9639 or (54-1)752-0021
Fax: (54-1)752-0021 or (54-1)752-9639
Email: dsanchez@inti.gov.ar
Seq primer: T7.
Location/Qualifiers
1. 390

/organism="Trypanosoma cruzi"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="2662"
/clone_lib="T. cruzi epimastigote normalized cDNA Library"
/cell_type="epimastigote"
/note="cDNA library constructed with oligo dT primed
epimastigote mRNA and cloned in pT7318D phagemid with
modified polylinker (PHARMACIA)"
BASE COUNT 93 a 105 c 95 g 91 t 6 others
ORIGIN

FEATURES

source

Query Match 79.0%; Score 15.8; DB 10; Length 390;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 tacggcaatgtaccagctg 20
|||||
Db 122 TAGGCAAGGCACAGCTG 140

RESULT 9
BE857550/c
LOCUS

DEFINITION
7901f06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305219 3'
BE857550
LOCUS
DEFINITION


```
||||| | |||||
Db 326 TACGGCATTTTACCAGCTG 344

RESULT 14
LOCUS BF009521/c
DEFINITION ss91h03.y1 Gm-cl064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
ACCESSION Gm-cl064-1518 5', mRNA sequence.
VERSION BF009521
KEYWORDS EST.
SOURCE BF009521.1 GI:10709797
ORGANISM soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 472)
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 452.
FEATURES
Location/Qualifiers
1..472
Source
/organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl064-1518"
/clone_lib="Gm-cl064"
/tissue_type="seedling epicotyls"
/dev_stage="2 week old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seedling for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT)
sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT 136 a 88 c 103 g 145 t
ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 472;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

||||| | |||||
Db 326 TACGGCATTTTACCAGCTG 344

RESULT 15
LOCUS AZ215252
DEFINITION Sheared DNA-105B6.TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION Sheared DNA-105B6, DNA sequence.
VERSION AZ215252
KEYWORDS GSS.
SOURCE AZ215252.1 GI:8432975
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 602)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J.,
Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Contact: Naji M. El-Sayed
Other_GSSs: Sheared DNA-105B6.TF
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mbd/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
FEATURES
Location/Qualifiers
1..602
Source
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-105B6"
/clone_lib="Sheared DNA"
/notes="Vector: pUC18; Site_1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Borell, Oxford University
Press, 1999)."
BASE COUNT 143 a 153 c 150 g 156 t
ORIGIN

Query Match 79.0%; Score 15.8; DB 13; Length 602;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

||||| | |||||
Db 203 TACGGCAAGGTACCAGCTG 221

Query Match 79.0%; Score 15.8; DB 13; Length 602;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: December 19, 2001, 17:00:29
Job time: 2271 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 16:22:43 ; Search time 230.16 Seconds
(without alignments)
74.498 Million cell updates/sec

Title: us-09-698-903b-7

Perfect score: 20
Sequence: 1 ctacggcaatgtaccagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428562619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_l101.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.*
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13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAH25428	PCR primer for the
2	20	100.0	20	AAD06996	PCR primer MDS258
3	20	100.0	415	AAD06997	Right (5') border
4	20	100.0	416	AAD06999	Left (3') border f
5	20	100.0	1037	AAQ04705	USP-Promoter-Casse
6	20	100.0	1085	AAQ04703	Legumin-signalpept
7	20	100.0	1160	AAQ04706	USP-signalpeptide
8	20	100.0	1166	AAQ04704	USP-Promoter-casse
9	20	100.0	1186	AAQ25707	Chimeric neo gene
10	20	100.0	1303	AAAT39337	Plasmid pTS88 (Eco
11	20	100.0	3153	AAAT29122	Plasmid DV131 comp

12	20	100.0	3201	12	AAQ14529	PPS029 Bt ICP codi
13	20	100.0	3201	12	AAQ15144	pVE36 Bt ICP codin
14	20	100.0	3336	21	AAAT29121	Plasmid DV130 comp
15	20	100.0	3694	21	AAAT29124	Plasmid DV133 used
16	20	100.0	3877	21	AAAT29123	Plasmid DV133 used
17	20	100.0	4832	22	AAH25423	Nucleotide sequenc
18	20	100.0	4946	18	AAAT59531	T-DNA of plasmid p
19	20	100.0	4946	22	AAH25422	Nucleotide sequenc
20	20	100.0	5228	22	AAH25422	Plasmid pTS172delt
21	20	100.0	5349	19	AAV23239	T-DNA of pTS24.
22	20	100.0	5864	17	AAAT39339	Plasmid pTCO113 T-
23	20	100.0	5864	17	AAAT39339	Plasmid pTCO113 T-
24	20	100.0	5865	22	AAD06990	Chimeric T-DNA of
25	20	100.0	5865	22	AAD06990	E. coli plasmid pT
26	20	100.0	6539	21	AAAT91097	Plasmid pTS174 use
27	20	100.0	6548	17	AAAT39336	Plasmid pTS172. C
28	20	100.0	6548	18	AAAT61394	E. coli plasmid pT
29	20	100.0	6548	21	AAAT91096	Plasmid pTS346. U
30	20	100.0	7492	22	AAAT6441	Plasmid pPS0212 co
31	20	100.0	7566	14	AAQ42160	Nucleotide sequenc
32	20	100.0	7599	22	AAAT25320	Plasmid pJD884 con
33	20	100.0	7639	14	AAQ42159	Sequence of opine
34	20	100.0	24593	6	AAAT50226	Complete nucleotid
35	20	100.0	24596	6	AAAT50182	Transformed Arabid
36	19	95.0	19	20	AAAT28157	Right flanking reg
37	18.4	92.0	1077	22	AAAT25439	T-DNA right border
38	18	90.0	21	22	AAAT89355	PCR primer for the
39	18	90.0	22	22	AAAT25438	PCR primer MDS193
40	18	90.0	22	22	AAD06995	p302 EcoRI primer
41	17	85.0	20	21	AAAT88410	Human 5' EST Isola
42	15.8	79.0	309	21	AAAT42531	Nucleotide sequenc
43	15.8	79.0	1290	21	AAAT59486	Human cDNA sequenc
44	15.8	79.0	4828	22	AAAT18238	Enterococcus faeca
45	15.4	77.0	11871	20	AAAT13108	

ALIGNMENTS

RESULT 1
AAH25428
ID AAH25428 standard; DNA; 20 BP.
XX
AC AAH25428;
XX
DT 22-AUG-2001 (first entry)
XX
DE PCR primer for the right border in transgenic plant MS-BN1.
XX
KW Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene;
KW fertility restorer gene; barnase gene; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200141558-Al.
XX
PD 14-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-EPI2872.
XX
PR 08-DEC-1999; 99US-0457037.
XX
XX (AVET) AVENTIS CROPS SCIENCE NV.
XX
XX De Both G, De Beuckeleer M;
XX
XX Left (3') border f
XX
XX USP-Promoter-Casse
XX
XX Legumin-signalpept
XX
XX USP-signalpeptide
XX
XX USP-Promoter-casse
XX
XX Chimeric neo gene
XX
XX Plasmid pTS88 (Eco
XX
XX Plasmid DV131 comp

Transgenic winter oilseed rape plants suited for producing hybrid seed
with improved qualities, comprises a male-sterility gene and fertility
restorer gene, integrated into the genome -
Example 4; Page 43; 98pp; English.

XX The specification describes a pair of transgenic winter oilseed rape
 CC plants suited for producing hybrid seed. One of the plants has an
 CC expression cassette comprising a male-sterility gene (e.g. barnase
 CC gene), and the other plant has an expression cassette comprising a
 CC fertility restorer gene (e.g. barstar gene), integrated into the genome.
 CC The fertility restorer gene is capable of preventing the activity of the
 CC male-sterility gene. The plant pair is useful for producing hybrid seed.
 CC Plants developed from the hybrid seed have agronomic performance
 CC genetic stability and adaptability to different genetic backgrounds.
 CC PCR primers AAB25427-28 were used to amplify the right border of
 CC a vector in a transgenic plant which carries the TA29-barnase
 CC transgene.

XX Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacggcaatgtaccagctg 20
 |||||
 Db 1 ctacggcaatgtaccagctg 20

RESULT 2

XX AAD06996
 ID AAD06996 standard; DNA; 20 BP.

XX AAD06996;

XX 06-AUG-2001 (first entry)

XX PCR primer MDB258 to generate the flanking region of elite event MS-B2.

XX MS-B2 elite event; transgenic Brassica plant; transformation event;
 XX male-sterility gene; PCR primer; thermal asymmetric interlaced;
 XX TAIL; ss.

XX Agrobacterium sp.

XX WO200131042-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-EP10680.

XX 29-OCT-1999; 99US-0430497.

XX (AVET) AVENTIS CROPS SCIENCE NV.

XX Weston B, De Beuckeleer M;

XX WPI; 2001-300517/31.

XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
 PT harboring specific transformation events, particularly by presence of
 PT male-sterility gene, at specific location in its genome -

XX Example 3; Page 28; 53pp; English.

XX The present invention relates to a transgenic Brassica plant or its
 CC seed, cells or tissues, characterised by harbouring a specific
 CC transformation event, particularly by the presence of a male-sterility
 CC gene, at a specific location in the Brassica genome. Transgenic
 CC Brassica plant is useful for producing a hybrid seed by crossing the
 CC transgenic plant with a male-fertile Brassica plant and harvesting the
 CC hybrid seed from the transgenic Brassica plant.
 CC The present sequence is tertiary thermal interlaced (TAIL)-PCR primer
 CC MDB258 used to right (5') and left (3') border flanking region of elite
 CC event MS-B2. This primer corresponds to position 224-243 of plasmid
 CC pTColl3.

XX SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacggcaatgtaccagctg 20
 |||||
 Db 1 ctacggcaatgtaccagctg 20

RESULT 3

XX AAD06997/c
 ID AAD06997 standard; DNA; 415 BP.

XX AAD06997;

XX 06-AUG-2001 (first entry)

XX Right (5') border flanking region of elite event MS-B2.

XX MS-B2 elite event; transgenic Brassica plant; transformation event;
 XX male-sterility gene; ds.

XX Chimeric - Agrobacterium sp.

XX Chimeric - Brassica sp.

XX Key Location/Qualifiers

FT misc_feature 1..234

FT /tag= a

FT /note= "Corresponds to plant DNA"

FT misc_feature 235..415

FT /tag= b

FT /note= "Corresponds to T-DNA"

XX WO200131042-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-EP10680.

XX 29-OCT-1999; 99US-0430497.

XX (AVET) AVENTIS CROPS SCIENCE NV.

XX Weston B, De Beuckeleer M;

XX WPI; 2001-300517/31.

XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
 PT harboring specific transformation events, particularly by presence of
 PT male-sterility gene, at specific location in its genome -

XX Claim 11; Page 51; 53pp; English.

XX The present invention relates to a transgenic Brassica plant or its
 CC seed, cells or tissues, characterised by harbouring a specific
 CC transformation event, particularly by the presence of a male-sterility
 CC gene, at a specific location in the Brassica genome. Transgenic
 CC Brassica plant is useful for producing a hybrid seed by crossing the
 CC transgenic plant with a male-fertile Brassica plant and harvesting the
 CC hybrid seed from the transgenic Brassica plant.
 CC The present sequence is right (5') border flanking region of elite event
 CC MS-B2.

XX Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 415 CTACGGCAATGTACCAGCTG 396

RESULT 4
AAD06999
ID AAD06999 standard; DNA; 416 BP.
XX AC AAD06999;
XX DT 06-AUG-2001 (first entry)
XX DE Left (3') border flanking region of elite event MS-B2.
XX KW MS-B2 elite event; transgenic Brassica plant; transformation event;
XX KW male-sterility gene; ds.
XX OS Chimeric - Agrobacterium sp.
XX OS Chimeric - Brassica sp.
XX FH Key Location/Qualifiers
FT misc_feature 1..193
FT /*tag= a
FT /note= "Corresponds to T-DNA"
FT misc_feature 194..416
FT /*tag= b
FT /note= "Corresponds to plant DNA"
XX WO200131042-A2.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-EP10680.
XX 29-OCT-1999; 99US-0430497.
XX (AVET ) AVENTIS CROPS SCIENCE NV.
XX Weston B, De Beuckeleer M;
XX WPI; 2001-300517/31.
XX Transgenic Brassica plants, seeds, cells or tissues, characterized by
PT harboring specific transformation events, particularly by presence of
PT male-sterility gene, at specific location in its genome -
XX Claim 11; Page 52; 53pp; English.
XX The present invention relates to a transgenic Brassica plant or its
CC seed, cells or tissues, characterised by harbouring a specific
CC transformation event, particularly by the presence of a male-sterility
CC gene, at a specific location in the Brassica genome. Transgenic
CC Brassica plant is useful for producing a hybrid seed by crossing the
CC transgenic plant with a male-fertile Brassica plant and harvesting the
CC hybrid seed from the transgenic Brassica plant.
CC The present sequence is left (3') border flanking region of elite event
CC MS-B2.
XX Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;

Query Match 100.0%; Score 20; DB 22; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 1 ctacggcaatgtaccagctg 20

RESULT 5

```

```

AAQ04705
ID AAQ04705 standard; DNA; 1037 BP.
XX AC AAQ04705;
XX DT 12-OCT-1990 (first entry)
XX DE USP-Promoter-cassette USP-Pr.T7.1.
XX KW Foreign DNA incorporation; recombinant DNA techniques;
XX KW higher plant genome; legumin; USP-Pr.T7-1; ss.
XX PN DE3920034-A.
XX 31-MAY-1990.
XX 20-JUN-1989; 89DE-3920034.
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp; German.
XX The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
CC HindIII-Ort in the 3' polylinker (1032-1037) for cloning the
CC cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
CC transfected.
CC See also AAQ04703-Q04706.
XX Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
   |||||
Db 841 ctacggcaatgtaccagctg 860

RESULT 6
AAQ04703
ID AAQ04703 standard; DNA; 1085 BP.
XX AC AAQ04703;
XX DT 12-OCT-1990 (first entry)
XX DE Legumin-signalpeptide cassette Le-Sig.T7.
XX KW Foreign DNA incorporation; recombinant DNA techniques;
XX KW higher plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
XX FH Key Location/Qualifiers
FT CDS 747..814
FT /*tag= a
FT /product=Legumin-signalpeptide
XX DE3920034-A.
XX 31-MAY-1990.
XX 20-JUN-1989; 89DE-3920034.
XX

```

```

PR 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX P-PSDB; AAR05198.
XX
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The legumin gene B4 is used. The unique BglII-Ort (815-820) site is for
XX ligating foreign DNA and the HindIII-Ort in the 3' polylinker
XX (1080-1085) for cloning the cassette in the Ti-vector pGA471.
XX The cassette is cloned into the binary Ti-vectors pGA471 and
XX Agrobacterium tumefaciens is transfected.
XX See also AAQ04703-Q04706.
XX
XX Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1085;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 889 ctacggcaatgtaccagctg 908
|||||

RESULT 7
AAQ04706
ID AAQ04706 standard; DNA; 1160 BP.
XX
XX AAQ04706;
XX
XX 12-OCT-1990 (first entry)
XX USP-signalpeptide cassette USP-Sig.T7.
XX Foreign DNA incorporation; recombinant DNA techniques;
XX higher plant genome; signalpeptide; USP-Sig.T7.; ss.
XX
XX Key Location/Qualifiers
XX CDS 708..877
XX /*tag= a
XX /product=signalpeptide
XX 747..817
XX Intron
XX
XX DE3920034-A.
XX
XX 31-MAY-1990.
XX
XX 20-JUN-1989; 89DE-3920034.
XX
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX P-PSDB; AAR05199.
XX
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The unique BglII-Ort (890-895) site is for

```

```

CC ligating foreign DNA and the HindIII-Ort in the 3' polylinker
CC (1155-1160) for cloning the cassette in the Ti-vector pGA471.
CC The cassette is cloned into the binary Ti-vectors pGA471 and
CC Agrobacterium tumefaciens is transfected.
CC See also AAQ04703-Q04706.
XX
XX Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1160;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 964 ctacggcaatgtaccagctg 983
|||||

RESULT 8
AAQ04704
ID AAQ04704 standard; DNA; 1166 BP.
XX
XX AAQ04704;
XX
XX 12-OCT-1990 (first entry)
XX USP-Promoter-cassette USP-Pr.T7.2.
XX Foreign DNA incorporation; recombinant DNA techniques;
XX higher plant genome; legumin; USP-Pr.T7-2; ss.
XX
XX DE3920034-A.
XX
XX 31-MAY-1990.
XX
XX 20-JUN-1989; 89DE-3920034.
XX
XX 19-SEP-1988; 88DD-0319887.
XX (PFLA-) VE KOMB PFLANZENZUC.
XX Bassuner R, Baumlein H, Muntz K, Hai NV, Wobus U;
XX WPI; 1990-172459/23.
XX Incorporation of DNA into higher plant genome - by specified
XX recombinant DNA techniques.
XX Disclosure; ; pp: German.
XX
XX The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
XX HindIII-Ort in the 3' polylinker (1261-1266) for cloning the
XX cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
XX transfected.
XX See also AAQ04703-Q04706.
XX
XX Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0 other;

Query Match 100.0%; Score 20; DB 11; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
Db 1070 ctacggcaatgtaccagctg 1089
|||||

RESULT 9
AAQ25707
ID AAQ25707 standard; DNA; 1186 BP.
XX
XX AAQ25707;

```

```
XX 07-DEC-1992 (first entry)
XX Chimeric neo gene probe.
XX Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX promoter 1..8
XX /tag= a
XX /note= "sequence derived from tapetum specific
XX promoter of Nicotiana tabacum"
XX CDS 9..790
XX /tag= b
XX /product= neomycine_phosphotransferase
XX misc_feature 791..1186
XX /tag= c
XX /note= "3' regulatory sequence contg. the
XX polyadenylation site derived from
XX Agrobacterium T-DNA gene 7"
XX PN W09209696-A.
XX 11-JUN-1992.
XX 21-NOV-1991; 91WO-EP02198.
XX 23-NOV-1990; 90EP-0403332.
XX 08-JUL-1991; 91EP-0401888.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX Dhalluin K, Goebel E;
XX WPI; 1992-217075/26.
XX Transforming monocotyledonous plants e.g. cereals - comprises
XX wounding and/or degrading cells of intact plant tissue or
XX embryogenic callus
XX Disclosure; Page 60; 76pp; English.
XX Two transformed corn plants were analysed by means of Southern
XX hybridisation. As a probe, a 1184 bp EcoRI-HindIII fragment derived
XX from another plasmid was used. The sequence of that plasmid is
XX given below. Results showed that at least a chimeric neo gene was
XX integrated into the plant genomic DNA.
XX SQ Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 1186;
XX Best Local Similarity 100.0%; Pred. No. 0.44;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ctacggcaatgtaccagctg 20
XX |
XX Db 1033 ctacggcaatgtaccagctg 1052
XX
XX RESULT 10
XX AAT39337
XX ID AAT39337 standard; DNA; 1303 BP.
XX AC AAT39337;
XX XX
XX 22-JAN-1997 (first entry)
XX DE Plasmid pTS88 (EcoRI-HindIII fragment).
XX XX
XX Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
```

```
KW transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_feature 1..35
XX /tag= a
XX /label= pGEM2
XX /note= "polylinker of pGEM2"
XX promoter 36..694
XX /tag= b
XX /label= p35S
XX /function= 35S promoter of cauliflower mosaic virus
XX strain CM1841
XX CDS 695..967
XX /tag= c
XX /label= barstar
XX /product= Bacillus amyloliquefaciens barstar
XX polyA_signal 968..1287
XX /tag= d
XX /label= 3'g7
XX /function= region containing polyadenylation signal
XX of gene 7 og Agrobacterium T-DNA
XX misc_feature 1288..1303
XX /tag= e
XX /label= pGEM2
XX /note= "polylinker of pGEM2"
XX W09626283-A1.
XX 29-AUG-1996.
XX 21-FEB-1996; 96WO-EP00722.
XX 21-FEB-1995; 95EP-0400364.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX Botterman J, Cornelissen M, Michiels F;
XX WPI; 1996-402373/40.
XX Prodn. of male sterile plants by transforming with a chimaeric
XX construct - comprising a male sterility DNA e.g. barnase and a
XX co-regulating gene, e.g. barstar, into the nuclear genome, useful
XX for generating hybrid cultivars
XX Example 1; Page 38; 56pp; English.
XX The HindIII-EcoRI fragment (AAT39337) of plasmid pTS88 contains
XX barstar DNA under control of a 35S promoter. The plasmid was
XX used with pTS174 (see also AAT39336) contg. barnase DNA under
XX control of the stamen-specific promoter EI to produce male sterile
XX rice cv. Kochihibiki transgenic plants, and with plasmid pV8136
XX (see also AAT39338) contg. barnase DNA under control of the stamen-
XX specific pCA55 promoter to produce male sterile maize plants.
XX Expression of barnase (a ribonuclease) in the stamen leads to male
XX sterility. Constitutive expression of barstar counteracts possible
XX low level expression of barnase DNA in non-stamen tissue.
XX SQ Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
```

```
Query Match 100.0%; Score 20; DB 17; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ctacggcaatgtaccagctg 20
XX |
XX Db 1098 ctacggcaatgtaccagctg 1117
XX
XX RESULT 11
```

```

AAZ29122
ID  AAZ29122 standard; DNA; 3153 BP.
AC  AAZ29122;
DT  21-FEB-2000 (first entry)
DE  Plasmid DV131 comprising L3/EGFP:NPTII/Tr7 expression cassette.
XX
XX  Transgenic seed; marker: aleurone-specific promoter; Plasmid DV131;
KW  GFP:NPTII fusion protein construct; L3/EGFP:NPTII/Tr7; maize R gene;
KW  expression cassette; maize L3 Oleosin gene; chimeric gene; transgene;
KW  MGFP:NPTII translational fusion; Tr7 terminator; luciferase gene; assay;
KW  Green fluorescent protein; GFP; gene fusion; selection; screening;
KW  expression; automated seed screening technique; screenable marker;
KW  transformant; embryogenic tissue; implementation; ds.
XX
XX  Synthetic.
OS
XX
XX  WO9960129-A1.
PN
XX
XX  25-NOV-1999.
PD
XX
XX  18-MAY-1999; 99WO-US11023.
PF
XX
XX  18-MAY-1998; 98US-0080625.
PR
XX
XX  (DEKA-) DEKALB GENETICS CORP.
PA
XX
XX  Kriz AL, Spencer TM;
PI
XX
XX  WPI; 2000-072441/06.
DR
XX
XX  Screenable marker genes useful for identification of transgenic seeds
PT  for plant breeding -
XX
XX  Example 1; Page 164-166; 182pp; English.
PS
XX
XX  The present DNA sequence is the plasmid DV131, that is used in the
CC  generation of GFP:NPTII fusion protein constructs. It contains an
CC  expression cassette comprising, a promoter from the maize L3 oleosin
CC  gene, the coding sequence of EGFP:NPTII translational fusion, excised
CC  from DV126 and the Tr7 terminator. This plasmid is used to carry a
CC  chimeric gene, comprising an aleurone-specific promoter like L3, that is
CC  operably linked to the gene encoding a screenable marker, like Green
CC  fluorescent protein (GFP), luciferase or maize R gene. The gene fusions
CC  allow both selection and screening of transformants. The aleurone-
CC  specific promoters direct the expression of the marker genes in
CC  embryonic tissues, allowing selection and screening of viable
CC  transgenic seeds. Screening of transgenic seeds avoids the need for
CC  growing and assaying of seeds for transgenes and allows implementation
CC  of automated seed screening techniques for the identification of
CC  transgenic seeds.
XX
XX  Sequence 3153 BP; 801 A; 857 C; 756 G; 739 T; 0 other;
SQ

Query Match      100.0%; Score 20; DB 21; Length 3153;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ctacggcaatgtaccagctg 20
    |||||
Db  2679 ctacggcaatgtaccagctg 2698

RESULT 12
AAQ14529
ID  AAQ14529 standard; DNA; 3201 BP.
XX
XX  AAZ14529;
AC
XX
XX  27-JAN-1992 (first entry)
DT

Query Match      100.0%; Score 20; DB 21; Length 3153;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ctacggcaatgtaccagctg 20
    |||||
Db  2679 ctacggcaatgtaccagctg 2698

RESULT 12
AAQ14529
ID  AAQ14529 standard; DNA; 3201 BP.
XX
XX  AAZ14529;
AC
XX
XX  27-JAN-1992 (first entry)
DT

```

```

XX  pPS029 Bt ICP coding sequence.
DE
XX
XX  Bacillus thuringiensis; insecticidal crystal protein; ICP;
KW  deletion; ss.
KW
XX
XX  Synthetic.
OS
XX
XX  WO9116432-A.
PN
XX
XX  31-OCT-1991.
PD
XX
XX  17-APR-1991; 91WO-EP00733.
PF
XX
XX  18-APR-1990; 90EP-0401055.
PR
XX
XX  (PLAN-) PLANT GENETIC SYST.
PA
XX
XX  Cornelissen M, Soetaert P, Stam M, Dockx J;
PI
XX
XX  WPI; 1991-339820/46.
DR
XX
XX  Modified Bacillus thuringiensis insecticidal crystal protein
PT  genes - having A and T sequences changed to G and C sequences
PT  encoding same amino acids, for increased expression levels
XX
XX  Disclosure; Fig 6(c); 78pp; English.
PS
XX
XX  "n" in the sequence refers to not known nucleotides.
CC
XX  pPS029 is identical to pVE36 (AAQ15144), but carries both the amino-
CC  terminal modification and the internal modification of the Bt ICP
CC  coding sequence.
CC
XX  See also AAQ14529, AAQ15142-44.
XX
XX  Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
SQ

Query Match      100.0%; Score 20; DB 12; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ctacggcaatgtaccagctg 20
    |||||
Db  2952 ctacggcaatgtaccagctg 2971

RESULT 13
AAQ15144
ID  AAQ15144 standard; DNA; 3201 BP.
XX
XX  AAZ15144;
AC
XX
XX  27-JAN-1992 (first entry)
DT
XX
XX  pVE36 Bt ICP coding sequence.
DE
XX
XX  Bacillus thuringiensis; insecticidal crystal protein; ICP;
KW  deletion; ss.
KW
XX
XX  Synthetic.
OS
XX
XX  WO9116432-A.
PN
XX
XX  31-OCT-1991.
PD
XX
XX  17-APR-1991; 91WO-EP00733.
PF
XX
XX  18-APR-1990; 90EP-0401055.
PR
XX
XX  (PLAN-) PLANT GENETIC SYST.
PA
XX
XX  Cornelissen M, Soetaert P, Stam M, Dockx J;
PI
XX

```


DR WPI; 1991-339820/46.

XX Modified *Bacillus thuringiensis* insecticidal crystal protein

PT genes - having A and T sequences changed to G and C sequences

PT encoding same amino acids, for increased expression levels

XX Disclosure; Fig 6(c); 78pp; English.

XX "n" in the sequence refers to not known nucleotides.

CC pPS029 (AAQ14529) is identical to pVE36, but carries both the amino-

CC terminal modification and the internal modification of the Bt ICP

CC coding sequence.

CC See also AAQ14529, AAQ15142-44.

XX Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;

SQ

Query Match 100.0%; Score 20; DB 12; Length 3201;

Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

QY 1 ctacggcaatgtaccagctg 20

Db 3025 ctacggcaatgtaccagctg 3044

|||||

RESULT 14

AAZ29121

ID AAZ29121 standard; DNA; 3336 BP.

XX

AC AAZ29121;

XX

DT 21-FEB-2000 (first entry)

XX

DE Plasmid DV130 comprising L3/MGFP:NPTII/Tr7 expression cassette.

XX

KW Transgenic seed; marker; aleurone-specific promoter; Plasmid DV130;

KW GFP:NPTII fusion protein construct; L3/MGFP:NPTII/Tr7; maize R gene;

KW expression cassette; maize L3 oleosin gene; chimeric gene; transgene;

KW MGFP:NPTII translational fusion; Tr7 terminator; luciferase gene;

KW Green fluorescent protein; GFP; gene fusion; selection; screening;

KW transformant; expression; automated seed screening technique; assay;

KW screenable marker; embryogenic tissue; implementation; ds.

XX

OS Synthetic.

XX

PN WO9960129-A1.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US11023.

XX

PR 18-MAY-1998; 98US-0080625.

XX

PA (DEKA-) DEKALB GENETICS CORP.

XX

PI Kriz AL, Spencer TM;

XX

WPI; 2000-072441/06.

XX

Screenable marker genes useful for identification of transgenic seeds

for plant breeding -

XX

Example 1; Page 163-164; 182pp; English.

XX

The present DNA sequence is the plasmid DV130, that is used in the

generation of GFP:NPTII fusion protein constructs. It contains an

expression cassette comprising, a promoter from the maize L3 oleosin

gene, the coding sequence of MGFP:NPTII translational fusion, excised

from DV127 and the Tr7 terminator. This plasmid is used to carry a

chimeric gene, comprising an aleurone-specific promoter like L3, that is

operably linked to a gene encoding a screenable marker, like Green

fluorescent protein (GFP), luciferase or maize R gene. The gene fusions

CC allow both selection and screening of transformants. The aleurone-

CC specific promoters direct the expression of the marker genes in

CC embryogenic tissues, allowing selection and screening of viable

CC transgenic seeds. Screening of transgenic seeds avoids the need for

CC growing and assaying of seeds for transgenes and allows implementation

CC of automated seed screening techniques for the identification of

CC transgenic seeds.

XX

SQ Sequence 3336 BP; 888 A; 830 C; 764 G; 854 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3336;

Best Local Similarity 100.0%; Pred. No. 0.5; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

QY 1 ctacggcaatgtaccagctg 20

Db 2862 ctacggcaatgtaccagctg 2881

|||||

RESULT 15

AAZ29124

ID AAZ29124 standard; DNA; 3694 BP.

XX

AC AAZ29124;

XX

DT 21-FEB-2000 (first entry)

XX

DE Plasmid DV133 used for construction of GFP:NPTII fusion protein.

XX

KW Transgenic seed; marker; aleurone-specific promoter; Plasmid DV133;

KW GFP:NPTII fusion protein construct; L3/rACT1 intron/EGFP:NPTII/Tr7;

KW expression cassette; maize L3 oleosin gene; chimeric gene; transgene;

KW EGFP:NPTII translational fusion; Tr7 terminator; luciferase gene;

KW Green fluorescent protein; GFP; gene fusion; maize R gene; selection;

KW screenable marker; screening; automated seed screening technique; assay;

KW transformant; expression; embryogenic tissue; implementation; ds.

XX

OS Synthetic.

XX

PN WO9960129-A1.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US11023.

XX

PR 18-MAY-1998; 98US-0080625.

XX

PA (DEKA-) DEKALB GENETICS CORP.

XX

PI Kriz AL, Spencer TM;

XX

WPI; 2000-072441/06.

XX

Screenable marker genes useful for identification of transgenic seeds

for plant breeding -

XX

Example 1; Page 168-170; 182pp; English.

XX

The present DNA sequence is the plasmid DV133, comprising

L3/rACT1 intron/EGFP:NPTII/Tr7, that is used in the generation of

GFP:NPTII fusion protein constructs. It contains an expression cassette

comprising, a promoter from the maize L3 oleosin gene, the rice actin 1

intron, the coding sequence of EGFP:NPTII translational fusion, excised

from DV126 and the Tr7 terminator. This plasmid is used to carry a

chimeric gene, comprising an aleurone-specific promoter like L3, that is

operably linked to a gene encoding a screenable marker, like Green

fluorescent protein (GFP), luciferase or maize R gene. The gene fusions

allow both selection and screening of transformants. The aleurone-

CC specific promoters direct the expression of the marker genes in

CC embryogenic tissues, allowing selection and screening of viable

CC transgenic seeds. Screening of transgenic seeds avoids the need for

CC growing and assaying of seeds for transgenes and allows implementation

CC of automated seed screening techniques for the identification of
 CC transgenic seeds.

XX
 SQ Sequence 3694 BP; 890 A; 984 C; 914 G; 906 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3694;
 Best Local Similarity 100.0%; Pred. NO. 0.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
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 Db 3220 ctacggcaatgtaccagctg 3239

Search completed: December 19, 2001, 17:31:51
 Job time: 4148 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

EM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 16:22:38 ; Search time 1631.12 Seconds
(without alignments)
202.280 Million cell updates/sec

Title: US-09-698-903B-7

Perfect score: 20
Sequence: 1 ctacggcaatgtaccagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:**

- 1: gb_ba:**
- 2: gb_htg:**
- 3: gb_in:**
- 4: gb_om:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pl:**
- 9: gb_pr:**
- 10: gb_ro:**
- 11: gb_sts:**
- 12: gb_sy:**
- 13: gb_un:**
- 14: gb_vi:**
- 15: em_ba:**
- 16: em_fun:**
- 17: em_hum:**
- 18: em_in:**
- 19: em_om:**
- 20: em_or:**
- 21: em_ov:**
- 22: em_pat:**
- 23: em_ph:**
- 24: em_pl:**
- 25: em_ro:**
- 26: em_sts:**
- 27: em_sy:**
- 28: em_un:**
- 29: em_vi:**
- 30: em_htgo_hum:**
- 31: em_htgo_inv:**
- 32: em_htgo_rod:**
- 33: em_htg_hum:**
- 34: em_htg_inv:**
- 35: em_htg_rod:**
- 36: em_htg_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX127754 Sequence
2	20	100.0	20	6	AX172448 Sequence
3	20	100.0	249	12	X05579 Soybean bet
c	4	20	100.0	415	6 AX127755 Sequence
	5	20	100.0	416	6 AX127757 Sequence
	6	20	100.0	831	1 ATTN7
	7	20	100.0	878	1 ATTN7
	8	20	100.0	1037	6 A10942
	9	20	100.0	1085	6 A10939
	10	20	100.0	1160	6 A10943
	11	20	100.0	1166	6 A10941
	12	20	100.0	1186	6 A18051
	13	20	100.0	1186	6 AR095107
	14	20	100.0	1186	6 AR098313
	15	20	100.0	1186	6 AX012338
	16	20	100.0	1186	6 I49886
	17	20	100.0	1186	6 I82374
c	18	20	100.0	2476	12 TBI251013
	19	20	100.0	3200	6 I44104
	20	20	100.0	3201	6 I44103
c	21	20	100.0	3236	12 TBI251014
	22	20	100.0	4832	6 AX172441
c	23	20	100.0	4946	6 A60108
c	24	20	100.0	4946	6 A76915
c	25	20	100.0	4946	6 AR098307
c	26	20	100.0	4946	6 AX172440
c	27	20	100.0	5349	6 A71437
c	28	20	100.0	5560	6 A60112
c	29	20	100.0	5560	6 AR098311
c	30	20	100.0	5865	6 AX127748
c	31	20	100.0	5865	6 AX127748
	32	20	100.0	6539	6 E31991
	33	20	100.0	6548	6 A60109
	34	20	100.0	6548	6 A76916
	35	20	100.0	6548	6 AR098308
	36	20	100.0	6548	6 E31990
	37	20	100.0	7566	6 A24783
	38	20	100.0	7566	6 AR074388
	39	20	100.0	7599	6 AX063413
	40	20	100.0	7639	6 A24782
	41	20	100.0	7639	6 AR074387
c	42	20	100.0	7811	6 AR078675
c	43	20	100.0	12095	12 BINHYGDNA
c	44	20	100.0	24595	1 ATACH5
c	45	20	100.0	24595	6 E00404

ALIGNMENTS

RESULT 1	AX127754	Sequence 7 from Patent WO0131042.	20 bp	DNA	PAT	15-MAY-2001
LOCUS	AX127754	Sequence 7 from Patent WO0131042.				
DEFINITION	AX127754	Sequence 7 from Patent WO0131042.				
ACCESSION	AX127754	Sequence 7 from Patent WO0131042.				
VERSION	AX127754.1	GI:14134401				
KEYWORDS		synthetic construct.				
SOURCE		artificial construct.				
ORGANISM		artificial sequence.				
REFERENCE		1 (bases 1 to 20)				
AUTHORS		Weston,B. and de Beuckeleer,M.				
TITLE		Male-sterile brassica plants and methods for producing same				
JOURNAL		Patent: WO 0131042-A 7 03-MAY-2001;				
FEATURES		Aventis CropScience N.V. (BE)				
source		Location/Qualifiers				
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		/organism="synthetic construct"				
		/db_xref="taxon:32630"				
		/note="primer M8258"				

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1 CTACGGCAATGTACCAGCTG 20

RESULT 2
AX172448
LOCUS AX172448 20 bp DNA PAT 03-JUL-2001
DEFINITION Sequence 9 from Patent WO0141558.
ACCESSION AX172448
VERSION AX172448.1 GI:14597560
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 20)
AUTHORS de Both.G. and de Beuckeleer,M.
TITLE Hybrid winter oilseed rape and methods for producing same
JOURNAL Patent: WO 0141558-A 9 14-JUN-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
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/db_xref="taxon:32630"
/notes="primer 258"
BASE COUNT      5 a      6 c      5 g      4 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1 CTACGGCAATGTACCAGCTG 20

RESULT 3
ARGMTUB
LOCUS ARGMTUB 249 bp DNA SYN 02-APR-1988
DEFINITION Soybean beta-1-tubulin gene fused to T1 plasmid unit 7 3UTR.
ACCESSION X05579
VERSION X05579.1 GI:58087
KEYWORDS beta-tubulin; fusion gene; plasmid.
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 249)
AUTHORS Guiltinan,M.J., Velten,J., Bustos,M.M., Cyr,R.J., Schell,J. and
Fosket,D.E.
TITLE The expression of a chimeric soybean beta-tubulin gene in tobacco
JOURNAL Mol. Gen. Genet. 207, 328-334 (1987)
FEATURES
source
1..249
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
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/codon_start=1
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/db_xref="GI:4376141"
/translation="AMAAWASSNWSTDPFMS"
CDS
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/notes="fusion product (17AA); Protein sequence is in
conflict with the conceptual translation"
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BASE COUNT      5 a      6 c      5 g      4 t
ORIGIN

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Best Local Similarity 100.0%; Score 20; DB 12; Length 249;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
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Db 110 CTACGGCAATGTACCAGCTG 129

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AX127755/c
LOCUS AX127755 415 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 8 from Patent WO0131042.
ACCESSION AX127755
VERSION AX127755.1 GI:14134402
KEYWORDS
SOURCE
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 415)
AUTHORS Weston,B. and de Beuckeleer,M.
TITLE Male-sterile brassica plants and methods for producing same
JOURNAL Patent: WO 0131042-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
1..415
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="5' border flanking region of elite event MS-B2"
1..234
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BASE COUNT      154 a      55 c      70 g      136 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 415 CTACGGCAATGTACCAGCTG 396

RESULT 5
AX127757
LOCUS AX127757 416 bp DNA PAT 15-MAY-2001
DEFINITION Sequence 10 from Patent WO0131042.
ACCESSION AX127757
VERSION AX127757.1 GI:14134404
KEYWORDS
SOURCE
synthetic construct.

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ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 416)
AUTHORS Weston,B. and de Beuckeleer,M.
TITLE Male-sterile brassica plants and methods for producing same
JOURNAL Patent: WO 0131042-A 10 03-MAY-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
1. .416
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="3' border flanking region of elite event MS-B2"
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misc_feature 194. .416
/note="plant DNA"
BASE COUNT 137 a 72 c 54 g 152 t 1 others
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTACGGCAATGTACCAGCTG 20
RESULT 6
LOCUS ATNRN7 831 bp DNA BCT 02-SEP-1999
DEFINITION Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for a
protein with unknown function.
ACCESSION V00090
VERSION V00090.1 GI:39180
KEYWORDS unidentified reading frame.
SOURCE Agrobacterium tumefaciens.
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 831)
AUTHORS Dhaese,P.; De Greve,H.; Gielen,J.; Seurinck,J.; Van Montagu,M.M.
and Schell,J.
TITLE Identification of sequences involved in the polyadenylation of
higher plant nuclear transcripts using Agrobacterium T-DNA genes as
models
JOURNAL EMBO J. 2, 419-426. (1983)
REFERENCE 2 (bases 76 to 100)
AUTHORS Dhaese,P.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-1983) to the EMBL/GenBank/DBJ databases
COMMENT Data kindly reviewed (27-MAY-1983) by Dhaese P.
FEATURES
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Location/Qualifiers
/organism="Agrobacterium tumefaciens"
/strain="(octopine T-DNA)"
/db_xref="taxon:358"
old_sequence 75. .81
/note="CG [1] revised CCAGAGG [2]"
/citation=[1]
/citation=[2]
old_sequence 99. .101
/note="CCA [1] revised CTA [2]"
/citation=[1]
/citation=[2]
mRNA 132. .673
/note="transcript 7 (alternate)"
mRNA 132. .672
/note="transcript 7"
CDS 148. .528
/note="unknown gene (148 is 1st base in codon) (525 is 3rd
base in codon)"

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/db_xref="SWISS-PROT:P03867"
/translation="MNFADTPLASLDLDWACEEFIKTYGASPOLETGEVQTNNGLLY
LYGKGLSQRHIDHLKFEKEELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PEKGFRLCHNRPFYPIVAHGSM"
BASE COUNT 262 a 176 c 138 g 255 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctg 20
|||||
Db 584 CTACGGCAATGTACCAGCTG 603
RESULT 7
LOCUS ATTDNA 878 bp DNA BCT 25-MAR-1996
DEFINITION Agrobacterium tumefaciens crown gall tumor T-DNA from T1 (tumor
inducing) plasmid pTiA6.
ACCESSION X00431
VERSION X00431.1 GI:39150
KEYWORDS plasmid.
SOURCE Agrobacterium tumefaciens.
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 878)
AUTHORS McPherson,J.C.
TITLE DNA sequence analysis of crown gall tumor T-DNA encoding the 0.7 kb
transcript
JOURNAL Nucleic Acids Res. 12 (5), 2317-2325 (1984)
MEDLINE 84169535
FEATURES
source
1. .878
Location/Qualifiers
/organism="Agrobacterium tumefaciens"
/strain="plasmid pTiA6"
/db_xref="taxon:358"
60. .66
/note="TATA-box"
misc_feature 68. .613
/note="polyadenylation signal"
CDS 109. .489
/note="unidentified reading frame"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacggcaatgtaccagctg 20
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Db 545 CTACGGCAATGTACCAGCTG 564

RESULT	8	Al0942	1037 bp	DNA	PAT	27-SEP-1993
LOCUS		Al0942	1037 bp	DNA	PAT	27-SEP-1993
DEFINITION		Nucleotide sequence 4 from patent number DE3920034.				
ACCESSION		Al0942				
VERSION		Al0942.1	GI:492369			
KEYWORDS		unidentified.				
SOURCE		unclassified.				
ORGANISM		1 (bases 1 to 1037)				
REFERENCE		Patent: DE 3920034-A 4 31-MAY-1990;				
AUTHORS		Location/Qualifiers				
JOURNAL		1..1037				
FEATURES		/organism="unidentified"				
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QY	1	ctacggcaatgtaccagctg 20				
DB	841	CTACGGCAATGTACCAGCTG 860				
RESULT	9	Al0939	1085 bp <td>DNA</td> <td>PAT</td> <td>27-SEP-1993</td>	DNA	PAT	27-SEP-1993
LOCUS		Al0939	1085 bp	DNA	PAT	27-SEP-1993
DEFINITION		Nucleotide sequence 1 from patent number DE3920034.				
ACCESSION		Al0939				
VERSION		Al0939.1	GI:492367			
KEYWORDS		unidentified.				
SOURCE		unclassified.				
ORGANISM		1 (bases 1 to 1085)				
REFERENCE		Patent: DE 3920034-A 1 31-MAY-1990;				
AUTHORS		Location/Qualifiers				
JOURNAL		1..1085				
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Matches		20; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	ctacggcaatgtaccagctg 20				
DB	889	CTACGGCAATGTACCAGCTG 908				
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LOCUS		Al0943	1160 bp	DNA	PAT	27-SEP-1993
DEFINITION		Nucleotide sequence 5 from patent number DE3920034.				
ACCESSION		Al0943				
VERSION		Al0943.1	GI:492370			
KEYWORDS		unidentified.				
SOURCE		unclassified.				
ORGANISM		1 (bases 1 to 1160)				
REFERENCE		Patent: DE 3920034-A 5 31-MAY-1990;				
AUTHORS						
JOURNAL						

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polyA_site
1055..1186
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polyadenylation site derived from agrobacterium T-DNA gene
7"

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Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1033 CTACGGCAATGTACCAGCTG 1052

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LOCUS          AR095107          1186 bp          DNA          PAT          08-SEP-2000
DEFINITION     Sequence 2 from patent US 6002070.
ACCESSION      AR095107
VERSION        AR095107.1 GI:10022665
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 1186)
AUTHORS        D'Halluin,K. and Gobel,E.
TITLE          Process for transforming monocotyledonous plants
JOURNAL        Patent: US 6002070-A 2 14-DEC-1999;
FEATURES       Location/Qualifiers
source         1..1186
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BASE COUNT    244 a    317 c    325 g    300 t
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Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 14
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DEFINITION     Sequence 2 from patent US 6074877.
ACCESSION      AR098313
VERSION        AR098313.1 GI:12807570
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 1186)
AUTHORS        D'Halluin,K. and Gobel,E.
TITLE          Process for transforming monocotyledonous plants
JOURNAL        Patent: US 6074877-A 2 13-JUN-2000;
FEATURES       Location/Qualifiers
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BASE COUNT    244 a    317 c    325 g    300 t
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS          AX012338          1186 bp          DNA          PAT          06-SEP-2000
DEFINITION     Sequence 2 from Patent EP0955371.
ACCESSION      AX012338
VERSION        AX012338.1 GI:9998387
KEYWORDS
SOURCE         synthetic construct.
ORGANISM       synthetic construct
               artificial sequence.
REFERENCE      1 (bases 1 to 1186)
AUTHORS        D'Halluin,K. and Goebel,E.D.
TITLE          Process for transforming monocotyledonous plants
JOURNAL        Patent: EP 0955371-A 2 10-NOV-1999;
FEATURES       Location/Qualifiers
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               /db_xref="taxon:32630"
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misc_feature   9..790
               /note="coding sequence of neomycine phosphotransferase"

misc_feature   791..1186
               /note="3', regulatory sequence containing the
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BASE COUNT    244 a    317 c    325 g    300 t
ORIGIN

Query Match    100.0%; Score 20; DB 6; Length 1186;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

Search completed: December 19, 2001, 17:27:49
Job time: 3911 sec
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; OTHER INFORMATION: /note= "sequence derived from
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; LOCATION: 791..1186
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; OTHER INFORMATION: T-DNA gene 7"
US-08-064-121-2

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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
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Db 1033 CTACGGCAATGTACCAGCTG 1052

```

```

RESULT 2
US-08-478-015-2
; Sequence 2, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,015
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: probe
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..8
; OTHER INFORMATION: /note= "sequence derived from
; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 9..790
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase ge
; FEATURE:
; NAME/KEY: -
; LOCATION: 791..1186
; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylat
; OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2

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```

Query Match 100.0%; Score 20; DB 1; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctg 20
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Db 1033 CTACGGCAATGTACCAGCTG 1052

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RESULT 3
US-08-475-975-2
; Sequence 2, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:

```

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/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 010830-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: probe
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..8
/ OTHER INFORMATION: /note= "sequence derived from
/ tapetum specific promoter of Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 9..790
/ OTHER INFORMATION: /label= NPTII
/ OTHER INFORMATION: /note= "coding sequence of neomycine
/ OTHER INFORMATION: phosphotransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 791..1186
/ OTHER INFORMATION: /label= 3'g7
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA gene 7"
/ US-08-475-973-2

Query Match 100.0%; Score 20; DB 3; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 4
US-09-084-889-2
/ Sequence 2, Application US/09084889
/ Patent No. 6074877
/ GENERAL INFORMATION:
/ APPLICANT: D'HALLUIN, Kathleen
/ APPLICANT: GOBEL, Elke
/ TITLE OF INVENTION: PROCESS FOR TRANSFORMING
/ TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: George Mason Bldg., Washington & Prince Sts.
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/084,889
/ FILING DATE:
/ CLASSIFICATION:
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/064,121
/ FILING DATE:
/ PRIOR APPLICATION DATA: EP 91401888.2
/ APPLICATION NUMBER:
/ FILING DATE: 08-JUL-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 010830-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-8620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: probe
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..8
/ OTHER INFORMATION: /note= "sequence derived from
/ tapetum specific promoter of Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 9..790
/ OTHER INFORMATION: /label= NPTII
/ OTHER INFORMATION: /note= "coding sequence of neomycine
/ OTHER INFORMATION: phosphotransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 791..1186
/ OTHER INFORMATION: /label= 3'g7
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA gene 7"
/ US-09-084-889-2

Query Match 100.0%; Score 20; DB 3; Length 1186;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 1033 CTACGGCAATGTACCAGCTG 1052

RESULT 5
US-08-894-440-2
/ Sequence 2, Application US/08894440
/ Patent No. 6025546
/ GENERAL INFORMATION:
/ APPLICANT: PLANT GENETIC SYSTEMS N.V.
/ TITLE OF INVENTION: Method to obtain male sterile plants
/ FILE REFERENCE: NMSCOR
/ CURRENT APPLICATION NUMBER: US/08/894,440
/ CURRENT FILING DATE: 1997-11-12
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1303
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HindIII-EcoRI
/ OTHER INFORMATION: fragment of pTS88
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefians
FEATURE:
NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1288)..(1303)
OTHER INFORMATION: polylinker of pGEM2
US-08-894-440-2
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Query Match      100.0%; Score 20; DB 3; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ctacggcaatgtaccagctg 20
      |||||
Db 1098 ctacggcaatgtaccagctg 1117
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```
RESULT 6
US-09-080-625-3
; Sequence 3, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; APPLICANT: Spencer, T. Michael
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; TITLE OF INVENTION: IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080.625
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Robert E.
; REGISTRATION NUMBER: P-42,628
; REFERENCE/DOCKET NUMBER: DEKM.161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
US-09-080-625-3
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Query Match      100.0%; Score 20; DB 4; Length 3153;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ctacggcaatgtaccagctg 20
      |||||
Db 2679 CTACGGCAATGTACCAGCTG 2698
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```
RESULT 7
US-08-453-104-23
; Sequence 23, Application US/08453104
; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453.104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
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Query Match      100.0%; Score 20; DB 1; Length 3200;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ctacggcaatgtaccagctg 20
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Db 2952 CTACGGCAATGTACCAGCTG 2971

RESULT 8
US-08-694-824-23
; Sequence 23, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,824
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-694-824-23

Query Match 100.0%; Score 20; DB 2; Length 3200;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 2952 CTACGGCAATGTACCAGCTG 2971

RESULT 9
US-08-453-104-22
; Sequence 22, Application US/08453104

; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2151..2155
; OTHER INFORMATION: /note= "Nucleotides 2151-2155
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-22

Query Match 100.0%; Score 20; DB 1; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 3025 CTACGGCAATGTACCAGCTG 3044

RESULT 10
US-08-694-824-22
; Sequence 22, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

;; TITLE OF INVENTION: IN PLANT CELLS
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Svecker & Mathis
;; STREET: George Mason Bldg., Washington & Prince Sts.
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/694,824
;; FILING DATE: 09-AUG-1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/937,869
;; FILING DATE: 16-DEC-1992
;; APPLICATION NUMBER: GB 90401055.0
;; FILING DATE: 18-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rea, Teresa S
;; REGISTRATION NUMBER: 30,427
;; REFERENCE/DOCKET NUMBER: 010830-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3201 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 2151..2155
;; OTHER INFORMATION: /note="Nucleotides 2151-2155
;; where N is not known."
US-08-694-824-22

Query Match 100.0%; Score 20; DB 2; Length 3201;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 3025 CTACGGCAATGTACCAGCTG 3044

RESULT 11
US-09-080-625-2
; Sequence 2, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; INFORMATION IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/080,625
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, Robert E.
;; REGISTRATION NUMBER: P-42,628
;; REFERENCE/DOCKET NUMBER: DEKM:161
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3336 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-09-080-625-2

Query Match 100.0%; Score 20; DB 4; Length 3336;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacggcaatgtaccagctg 20
|||||
Db 2862 CTACGGCAATGTACCAGCTG 2881

RESULT 12
US-09-080-625-5
; Sequence 5, Application US/09080625
; Patent No. 6307123
; GENERAL INFORMATION:
; APPLICANT: Kriz, Alan L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
; INFORMATION IDENTIFICATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,625
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Robert E.
; REGISTRATION NUMBER: P-42,628
; REFERENCE/DOCKET NUMBER: DEKM:161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-080-625-5

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RESULT 15
US-08-817-188-5/c
; Sequence 5, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366

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;; EARLIER FILING DATE: 1996-07-31
;; EARLIER APPLICATION NUMBER: EP 95401844.6
;; EARLIER FILING DATE: 1995-08-04
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 5560
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
;; OTHER INFORMATION: plasmid pTHW142
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(25)
;; OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
;; OTHER INFORMATION: pTB6S3
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (84)..(296)
;; OTHER INFORMATION: 3' g7: 3' untranslated region containing the
;; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
;; OTHER INFORMATION: T-DNA
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (318)..(869)
;; OTHER INFORMATION: Bar: region coding for phosphinotricin
;; OTHER INFORMATION: acetyltransferase
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (830)..(2760)
;; OTHER INFORMATION: PSSU: promoter region of Rubisco small subunit
;; OTHER INFORMATION: gene of Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2765)..(3058)
;; OTHER INFORMATION: 3' untranslated region of the CamV 35S transcript
;; OTHER INFORMATION: containing polyadenylation signals
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (3059)..(5056)
;; OTHER INFORMATION: uidA: region coding for beta-glucuronidase
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (4483)..(4671)
;; OTHER INFORMATION: IV2: region corresponding to the second intron of
;; OTHER INFORMATION: the St-LSI gene
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5067)..(5502)
;; OTHER INFORMATION: P35S: 35S promoter region of CamV
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5533)..(5560)
;; OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
;; OTHER INFORMATION: pTB6S3
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5058)..(5059)
;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5077)..(5078)
;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (5476)..(5479)
;; OTHER INFORMATION: region with unknown sequence (may contain up to 20
;; OTHER INFORMATION: nucleotides)
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US-08-817-188-5

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Query Match      100.0%; Score 20; DB 3; Length 5560;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||||||||||||||||
Db 230 CTACGGCAATGTACCAGCTG 211
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Search completed: December 19, 2001, 17:33:57
Job time: 4274 sec

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